

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:57:50 ; Search time 362 Seconds
(without alignments)
9501.607 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	854.4	44.2	1203	3	US-09-220-528-65
8	854.4	44.2	1203	3	US-09-949-016-3208
9	751.6	38.8	1271	3	US-09-187-906-18
10	751.6	38.8	1271	3	US-09-489-407-18
11	224.8	11.6	24984	3	US-09-949-016-14950
12	218.4	11.3	260	3	US-09-016-434-530
13	192.8	10.0	601	3	US-09-949-016-116675
14	169.8	8.8	238	3	US-09-016-434-537
15	102	5.3	1392	3	US-08-957-063-2
16	102	5.3	1392	3	US-09-487-685-2
17	102	5.3	1392	3	US-08-802-805D-2
18	102	5.3	1392	3	US-09-388-316C-2
19	102	5.3	1490	3	US-08-861-990-10
20	102	5.3	1888	3	US-09-187-906-12
21	102	5.3	1888	3	US-09-489-407-12
22	102	5.3	1995	3	US-08-957-063-15
23	102	5.3	1995	3	US-09-487-685-15
24	102	5.3	1995	3	US-08-802-805D-15

25	102	5.3	1995	3	US-09-388-316C-15	Sequence 15, Appl
26	102	5.3	2600	3	US-08-957-063-1	Sequence 1, Appl
27	102	5.3	2600	3	US-09-487-685-1	Sequence 1, Appl
28	102	5.3	2600	3	US-08-802-805D-1	Sequence 1, Appl
29	102	5.3	2600	3	US-09-388-316C-1	Sequence 1, Appl
30	88	4.5	670	3	US-08-957-063-19	Sequence 19, Appl
31	88	4.5	670	3	US-09-487-685-19	Sequence 19, Appl
32	88	4.5	670	3	US-08-802-805D-19	Sequence 19, Appl
33	88	4.5	670	3	US-09-388-316C-19	Sequence 19, Appl
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42	86	4.4	3358	3	US-08-957-063-4	Sequence 4, Appl
43	86	4.4	3358	3	US-09-487-685-4	Sequence 4, Appl
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ALIGNMENTS

RESULT 1
US-09-187-906-16
; Sequence 16, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1889 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

NAME/KEY: CDS
LOCATION: 41..1231

LOCATION:
US-09-187-906-16

Query Match 97.5%; Score 1887; DB 3; Length 1889;

Query Match 97.5%; Score 100%; DB 3; Version 1003;
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity 100.0%; Freq. NO. 0;
Matches 1887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db		
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Qy	ATGCGAGGCTAATCCCGTTGCAAGGTCCTCTACAGCACTGGGGTCTCTGCACTCTCCAG	288
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Db		
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Qy	AGAACAACTCAGGAACAGCTCTCTGTATAGACTGCAGGTGCCATCGGGCATGAAGACCCA	408
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Qy 1429 CQTCTGCTCCAGAAAGAGTCTTAGAAGTGAAGGCTGTGACCCCTCCGATCCTGAGCGCT 1488
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Qy 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887
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RESULT 3

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US-09-187-906-14
; Sequence 14, Application US/09187906
; Patent No. 6671135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..1242
; US-09-187-906-14

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: March 22, 2006, 08:37:22 ; Search time 9930 Seconds
(without alignments)
11076.745 Million cell updates/sec
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Sequence: 1 gaattggccctcgaggcca.....aaaaaaaaaaaaaaaaaaaaa 1935
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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3: gb_env.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	1887	97.5	1889 6 AR452126
7	1884	97.4	1884 9 AF051766
8	1871.8	96.7	2006 9 BC066202
9	1867	96.5	1867 9 AB008833
10	1867	96.5	1878 6 BD195078
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13	1379	71.3	2070 9 BC079378
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25	897.6	46.4	1699	6	AR452128	Sequence
26	854.4	44.2	1203	6	BD251402	Novel neu
27	852.8	44.1	1203	6	AX658358	Sequence
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29	851.4	44.0	1200	6	A92047	Sequence 1
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32	751.6	38.8	1271	6	AR452069	Sequence
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37	604.6	31.2	667	9	AF184920	Rattus no
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ALIGNMENTS

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LOCUS BD137007 GFR alpha 3 and its uses. 1935 bp DNA linear PAT 18-SEP-2002
DEFINITION GFR alpha 3 and its uses.
ACCESSION BD137007
VERSION BD137007.1 GI:23231952
KEYWORDS JP 2002507421-A/4.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1935)
SAUVAGE,F.J.D., KLEIN,R.D., PHILLIPS,H.S. and ROSENTHAL,A.
GFR alpha 3 and its uses
TITLE GFR alpha 3 and its uses
JOURNAL Patent: JP 2002507421-A 4 12-MAR-2002;
GENENTECH INC
COMMENT OS Mus musculus (mouse)
PN JP 2002507421-A/4
PD 12-MAR-2002
PF 19-MAR-1999 JP 2000538000
PR 23-MAR-1998 US 60/079124,13-APR-1998 US 60/081569 PI
FRDERIC J DE SAUVAGE, ROBERT D KLEIN, HEIDI S PHILLIPS, ARNON PI
ROSENTHAL
PC C12N15/09,A61K39/395,A61K45/00,A61P1/02,A61P1/10,A61P11/06, PC
A61P17/02,
PC A61P25/02,A61P25/06,A61P27/02,C07K14/71,C07K16/28,C07K19/00,
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GFR alpha 3 and its uses.
FH Key Location/Qualifiers
FT source 1..1935
FT /organism='Mus musculus (mouse)'.
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source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1935; DB 6; Length 1935;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAATTTGGCCCTCGAGGCGCAAGAAATTCGGCAGCAGCGGGCGGCCGCCAGGGCAGGAGGC 60
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QY 181 TGCCA CAGAGAACAGGTTTGTGAA CAGCTGTACCCAGGCGCAAGAAAGAAATGCGAGGCTAA 240
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QY 241 TCCCGCTTGCAGGCTGCTACCAAGCACTGGGGCTCTGCACTCCAGTTTAAAGCAGGCC 300
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QY 301 GCTGCCCTTAGAGGAGTGTGCATGTCTGCAGACTGCTAGAGGCGAGCAGAACTCAG 360
Db 301 GCTGCCCTTAGAGGAGTGTGCATGTCTGCAGACTGCTAGAGGCGAGCAGAACTCAG 360
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RESULT 2

MMTRNR3
LOCUS
DEFINITION Mus musculus mRNA for TGF-beta-related neurotrophic factor
receptor-3.
ACCESSION Y15110
VERSION Y15110.1
KEYWORDS GI:2959855
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

MMTRNR3 1932 bp mRNA linear ROD 03-MAR-1998
Mus musculus mRNA for TGF-beta-related neurotrophic factor
receptor-3.

Y15110.1 GI:2959855
neurotrophic receptor; TGF-beta related protein; tmR-3 gene.
Mus musculus (house mouse)
Mus musculus


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AF036163 1911 bp mRNA linear ROD 26-JUN-1998
LOCUS Mus musculus glial cell line-derived neurotrophic factor family
DEFINITION receptor alpha 3 (gfra3) mRNA, complete cds.
ACCESSION AF036163
VERSION AF036163.1 GI:2674176
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1911)
AUTHORS Naveilhan,P., Baudet,C., Mikaelis,A., Shen,L., Westphal,H. and
Ernfors,P.
Expression and regulation of GFRalpha3, a glial cell line-derived
neurotrophic factor family receptor
Proc. Natl. Acad. Sci. U.S.A. 95 (3), 1295-1300 (1998)
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2 (bases 1 to 1911)
AUTHORS Naveilhan,P. and Ernfors,P.
Direct Submission
Submitted (28-NOV-1997) Lab. Mol. Neuro. Dept. Medical Biochemistry
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RESULT 4
BD195079
LOCUS

BD195079 1889 bp DNA linear PAT 17-JUL-2003

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DEFINITION Ret ligand (RetL) for stimulating neural and renal growth.
ACCESSION BD195079
VERSION BD195079.1 GI:33004837
KEYWORDS JP 2002515743-A/10.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 1889)
AUTHORS Nadel,M.S., Hession,C. and Cate,R.L.
TITLE Ret ligand (RetL) for stimulating neural and renal growth
JOURNAL Patent: JP 2002515743-A 10 28-MAY-2002;
COMMENT BIOGEN INC
OS Unidentified
PN JP 2002515743-A/10
PD 28-MAY-2002
PF 07-MAY-1996 US 60/017427,07-JUN-1996 US 60/019300 PR
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16-JUL-1996 US 60/021859
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LQTLW"

ORIGIN

Query Match		97.4%;	Score 1884;	DB 9;	Length 1884;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1884;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	27	CGGACAGAGCGCGCGCGCCAGCGCAGGAGAGCGCTGTCGATCCCGGCGCTCCACCGG	86		
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QY	87	CAATGGGGCTCTCTGGAGCCCGGACCTTCCACTGCTGTGATGATCTCTGCTACTGTGTGT	146		
DB	61	CAATGGGGCTCTCTGGAGCCCGGACCTTCCACTGCTGTGATGATCTCTGCTACTGTGTGT	120		
QY	147	CGTTGTGGCTGCACTTGGAGCAGGAACTCCCTTGGCCACAGAGAACTGTTTGTGAACA	206		
DB	121	CGTTGTGGCTGCACTTGGAGCAGGAACTCCCTTGGCCACAGAGAACTGTTTGTGAACA	180		
QY	207	GCTGTACCCAGGCGAGAAAGAAATCGAGGCTAATCCCGCTTGGCAAGGCTGCTACCCAGC	266		
DB	181	GCTGTACCCAGGCGAGAAAGAAATCGAGGCTAATCCCGCTTGGCAAGGCTGCTACCCAGC	240		
QY	267	ACCTGGGCTCTGCACTTCAATTAAGCAGCGCGTGCCTTTAGAGAGTCTGCAATGT	326		
DB	241	ACCTGGGCTCTGCACTTCAATTAAGCAGCGCGTGCCTTTAGAGAGTCTGCAATGT	300		
QY	327	CTGCAGACTGCTTAGAGGAGCAGAACTCAGGACAGCTCTCTGATAGACTGCAGGT	386		
DB	301	CTGCAGACTGCTTAGAGGAGCAGAACTCAGGACAGCTCTCTGATAGACTGCAGGT	360		
QY	387	GCATCGGGGCTAGAGCAACCAAGTACCTGTCTGGACATTTATTTGGACCGTTCAACCTG	446		
DB	361	GCATCGGGGCTAGAGCAACCAAGTACCTGTCTGGACATTTATTTGGACCGTTCAACCTG	420		
QY	447	CCCGAAGCCTTGGTGACTACGAGTTGGATGTCTACCTATGAAGACACAGTGACAGCA	506		
DB	421	CCCGAAGCCTTGGTGACTACGAGTTGGATGTCTACCTATGAAGACACAGTGACAGCA	480		
QY	507	AACTCTGGAAATGAATCTTAGCAAGTTGAAATGCTCAAAACAGACTCGGACCTTGC	566		
DB	481	AACTCTGGAAATGAATCTTAGCAAGTTGAAATGCTCAAAACAGACTCGGACCTTGC	540		
QY	567	TCAAATTTCTGTATGTGTACTCTTTCAGACAGTGTGACCGCTTGGCAAGGCTACG	626		
DB	541	TCAAATTTCTGTATGTGTACTCTTTCAGACAGTGTGACCGCTTGGCAAGGCTACG	600		
QY	627	GGGAGCAGTCTCAGGATTCGCTGCGAGCGCACTCTGCTAGCCGAGCTGCGCTCCT	686		
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QY	687	TCCTTTGAGAGGAGCAGAGTCCAGCTCAGGCTGCTGCTGTGCTGTGCTGTGACCCAG	746		
DB	661	TCCTTTGAGAGGAGCAGAGTCCAGCTCAGGCTGCTGCTGTGCTGTGCTGTGACCCAG	720		
QY	747	AAGATGCGGGCTGTGGGAGCGCGGTAACCAATCGCCCGCCAGTTGCGCCCTGCCTT	806		
DB	721	AAGATGCGGGCTGTGGGAGCGCGGTAACCAATCGCCCGCCAGTTGCGCCCTGCCTT	780		
QY	807	CTGTAAACCCCAATTGCTGTGATCTGCGGAGCTTCTGCGGTGCGAACCTTTGTGAGAT	866		
DB	781	CTGTAAACCCCAATTGCTGTGATCTGCGGAGCTTCTGCGGTGCGAACCTTTGTGAGAT	840		
QY	867	CACGCTGTAGTACCTTCCAGACCCCACTGTATCTATGACATCTTGGGACTTGTGCA	926		
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QY	97	CTGAGCAGTCCAGATGTCTGCGGGCATACCTTGGGGCTGATTGGGACTGCCATGACCCCAA	986
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QY	1107	AGGCAATTCAGCTAAGATGCTTTCACAGACAGCTTCTTCCAGAGCTTGGGAGACT	1166
DB	1081	AGGCAATTCAGCTAAGATGCTTTCACAGACAGCTTCTTCCAGAGCTTGGGAGACT	1140
QY	1167	CTACTTTTTCAGTGTGTCAGCAGCAGACAGCAACCCCTGCTGTGAGACTGCAGCCACGCG	1226
DB	1141	CTACTTTTTCAGTGTGTCAGCAGCAGACAGCAACCCCTGCTGTGAGACTGCAGCCACGCG	1200
QY	1227	TACCCATTTCTTTTCTTCTCCATCTCTTCCCTTGAATTTCTGCTGCAGACCTCTGTGAGCTGG	1286
DB	1201	TACCCATTTCTTTTCTTCTCCATCTCTTCCCTTGAATTTCTGCTGCAGACCTCTGTGAGCTGG	1260
QY	1287	GCTTCTCAGGGTCTTGTCTCTTCCACCAACCCAGACTGATTTTGAGCTGTGTGGTGG	1346
DB	1261	GCTTCTCAGGGTCTTGTCTCTTCCACCAACCCAGACTGATTTTGAGCTGTGTGGTGG	1320
QY	1347	GAGGAGACTCCCGCAGCTGTGGAGAGACGCGGTCTACACAGCAACCCGGAACCAA	1406
DB	1321	GAGGAGACTCCCGCAGCTGTGGAGAGACGCGGTCTACACAGCAACCCGGAACCAA	1380
QY	1407	CCAGGCAATTCGCGCAGCACAATCCGCTCTCTCCAGAGAGGCTTTAGAGAGTGAAGGCTGTG	1466
DB	1381	CCAGGCAATTCGCGCAGCACAATCCGCTCTCTCCAGAGAGGCTTTAGAGAGTGAAGGCTGTG	1440
QY	1467	ACCTTCCGATCTGAGGCGGTAGTTTTCAAACTCTTCCCTTGCCTGCTGCTTCTTCTGCT	1526
DB	1441	ACCTTCCGATCTGAGGCGGTAGTTTTCAAACTCTTCCCTTGCCTGCTGCTTCTTCTGCT	1500
QY	1527	CAGGCTGCTCTCTTAGGACTTTTGTGGTCCAGTTTGTGCTTCTGCTTCTGATGCTGAT	1586
DB	1501	CAGGCTGCTCTCTTAGGACTTTTGTGGTCCAGTTTGTGCTTCTGCTTCTGATGCTGAT	1560
QY	1587	AGCGGCTCACCTCCAGCGCTTCTTCTCTTCCAGAGACCAACCCAGAGGCTTAAGGAATCA	1646
DB	1561	AGCGGCTCACCTCCAGCGCTTCTTCTCTTCCAGAGACCAACCCAGAGGCTTAAGGAATCA	1620
QY	1647	GTCAATTCCTGTTGCTTCTCCAGAGAGGCTTAAGGTTTCTGAGGTGCTGAGAAAA	1706
DB	1621	GTCAATTCCTGTTGCTTCTCCAGAGAGGCTTAAGGTTTCTGAGGTGCTGAGAAAA	1680
QY	1707	ATGTTTCTTGTGTGGAGGCTGCTGCTCAGGCTCCAGCTTCTGATGGAAGATA	1766
DB	1681	ATGTTTCTTGTGTGGAGGCTGCTGCTCAGGCTCCAGCTTCTGATGGAAGATA	1740
QY	1767	AAAACTCTGCTGCTTGTGCTCTGCTCAGGCAATCTTCAAACTTTGGGCTCAAGAG	1826
DB	1741	AAAACTCTGCTGCTTGTGCTCTGCTCAGGCAATCTTCAAACTTTGGGCTCAAGAG	1800
QY	1827	CTAAGTCTTTGGGTCTTGTGTTTAACTTACTGTCTTCTTCTTCTTCTTCTTCTTCTTCT	1886
DB	1801	CTAAGTCTTTGGGTCTTGTGTTTAACTTACTGTCTTCTTCTTCTTCTTCTTCTTCTTCT	1860
QY	1887	GCTCATGATTAACATTTTGTGCTT	1910
DB	1861	GCTCATGATTAACATTTTGTGCTT	1884

RESULT 8
BC066202
LOCUS

BC066202 2006 bp mRNA linear ROD 08-MAR-2005

DEFINITION	Mus musculus glial cell line derived neurotrophic factor family receptor alpha 3, mRNA (cdna clone MGC:76710 IMAGE:6430904), complete cds.
ACCESSION	BC066202
VERSION	BC066202.1
KEYWORDS	GI:42490963
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2006) Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Ustin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PV, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KM, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettelman M, Madan A, Rodrigues S, Sanchez A, Whitting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smalusz DE, Schnurch A, Schein JF, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
CONSTRM	12477932
TITLE	2 (bases 1 to 2006) Director MGC Project.
JOURNAL	Direct Submission Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
PUBMED	NIH-MGC Project URL: http://mgc.nci.nih.gov
REFERENCE	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000) cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
REMARK	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 144 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31981761. Location/Qualifiers 1..2006 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="MGC:76710 IMAGE:6430904" /tissue_type="Pancreas, pooled libraries Melton normalized mixed mouse pancreas 1 Ni-MMS1, Amplified Melton mou se islets 1 M1S1-A, and Kaestner ngm3 wt."
FEATURES	1 /clone lib="NIH_MGC_137" /lab host="DH10B" /note="Vector: pSPORT1" 1..2006 /gene="Gfra3" /db_xref="GeneID:14587"
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gene	

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Query Match	96.7%	Score 1871.8	DB 9	Length 2006				
Best Local Similarity	99.4%	Pred. No. 0						
Matches 1879	Conservative 0	Mismatches 12	Indels 0	Gaps 0				
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DB	116	CGCGCGCCGCGAGCGAGCGAGCGCGTCTGCGCATCCCGGGGCGTCCACCGCGCATGGGGCT	175					
QY	97	CTCTGGAGCCGCGAGCCTCCACCTGCTGATGATCTGCTACTGTGCTGTGCTGTGCTGTGCT	156					
DB	176	CTCTGGAGCCGCGAGCCTCCACCTGCTGATGATCTGCTACTGTGCTGTGCTGTGCTGTGCT	235					
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DB	236	GCACCTTGAGCAGAGAAACTCCCTTGCCACAGAGAACAGGTTTGTGAACAGCTGTACCCA	295					
QY	217	GGCCAGAAAGAAATCGCAGGGCTAAATCCCGCTTGAAGGCTGCCTACAGACACTGGGCTC	276					
DB	296	GGCCAGAAAGAAATCGCAGGGCTAAATCCCGCTTGAAGGCTGCCTACAGACACTGGGCTC	355					
QY	277	CTGCACTCTCCAGTTTACGAGCGCGCTGCCCTTAGAGAGTCTGCCATGCTGCAGACTG	336					
DB	356	CTGCACTCTCCAGTTTACGAGCGCGCTGCCCTTAGAGAGTCTGCCATGCTGCAGACTG	415					
QY	337	CCTAGAGCAGCAGAACTCAGGAAACAGCTCTCTGATAGACTGCAGGTGCCATCGCGC	396					
DB	416	CCTAGAGCAGCAGAACTCAGGAAACAGCTCTCTGATAGACTGCAGGTGCCATCGCGC	475					
QY	397	CATGAAGCACCAGCTACCTGTCTGGACATTTATTATGACCGTTTCACTGCGCCGAGCGCT	456					
DB	476	CATGAAGCACCAGCTACCTGTCTGGACATTTATTATGACCGTTTCACTGCGCCGAGCGCT	535					
QY	457	TGGTGACTACAGGTTGGATGTCACCTCATGAAAGACACAGTGACCAAGCAACCTCGAA	516					
DB	536	TGGTGACTACAGGTTGGATGTCACCTCATGAAAGACACAGTGACCAAGCAACCTCGAA	595					
QY	517	AATGAATCTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAAATTGC	576					
DB	596	AATGAATCTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAAATTGC	655					
QY	577	TAATGCTGTGTACTTTCACGACAGTGTGACCGCTTGGCGAAGCGCTACCGGGAGGCATG	636					
DB	656	TAATGCTGTGTACTTTCACGACAGTGTGACCGCTTGGCGAAGCGCTACCGGGAGGCATG	715					
QY	637	CTCAGGGATCGCTGCCAGCGCACCTCTGCTTACGCCAGCTCGCGCTCTCTTTTGAGAA	696					
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QY	697	GGCAGCAGATGCCACGCTCAGGGTCTGCTGCTGTGCTTCTGTGTGACACAGAGATGCGGG	756					
DB	776	GGCAGCAGATGCCACGCTCAGGGTCTGCTGCTGTGCTTCTGTGTGACACAGAGATGCGGG	835					
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ORIGIN		
Query Match	96.7%; Score 1871.8; DB 9; Length 2006;	
Best Local Similarity	99.4%; Pred. No. 0;	
Matches 1879; Conservative	0; Mismatches 12; Indels 0; Gaps 0;	
QY	37 CGCGCGCCAGCGCAGCAGAGCGCTCTCGCATCCCGGGCGTCCACCCGCATGGGCT 96	
Db	116 CGCGCGCCAGCGCAGCAGAGCGCTCTCGCATCCCGGGCGTCCACCCGCATGGGCT 175	
QY	97 CTCTGGAGCGCGGACCTCCACTGCTGATGATCTCTGCTACTGCTGCTGCTGCTGCT 156	
Db	176 CTCTGGAGCGCGGACCTCCACTGCTGATGATCTCTGCTACTGCTGCTGCTGCTGCT 235	
QY	157 GCCACTTGGAGCAGGAAACTCCCTTGGCCACAGAGAAAGAGTTTGTGAACAGCTGTACCCA 216	
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QY	217 GGCAGAAAGAAATGCGAGGCTAATCCCGTTGCAAGCGTCCCTACACGACCTCGGGCTC 276	
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QY	637 CTCAGGATTCGCTGCCAGCGCACCTCTGCTAGCCACAGTGGCGTCTCTTTTGGAA 696	
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QY	697 GGCAGCAGATCCACAGCTCAGGGTCTGCTGCTGTGTCCCTGTGTGACCAAGAGATGCGGG 756	
Db	776 GGCAGCAGATCCACAGCTCAGGGTCTGCTGCTGTGTCCCTGTGTGACCAAGAGATGCGGG 835	
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Qy	937	CAGATGCTGGGGGATACCTGGGGCTGATTGGGACTGCCATGACCCCAACTTCATCAG		996
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Qy	1237	TTCTTTTCTCACTCCCTTGATTCTGCTGCAGACCTCTGGTAGCTGGGCTTCCTCAG		1296
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Qy	1717	TGTTGGAAGGCTGCTCTCCAGGCTCCAGTCCCTCTGAAATGGAAGATAAAGCCTGCT		1776
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LOCUS			complete cds.
DEFINITION			
ACCESSION			
VERSION			
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ORGANISM			
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AUTHORS			
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JOURNAL			
PUBMED			
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gene			
mRNA			
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ORIGIN			
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Best Local Similarity			
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QY 164 GGAGCAGGAAATCCCTTCCACAGAGAAACAGGTTTGTGAACAGCTGTACCCAGGCCAGA 223
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QY 224 AAGAAATGCGAGGCTAATCCCGCTTGCAGAGCTGCTACCAAGCACTCGGGCTCTGCACC 283
DB 181 AAGAAATGCGAGGCTAATCCCGCTTGCAGAGCTGCTACCAAGCACTCGGGCTCTGCACC 240
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DB 301 GCAGCAGAACTCAGGAAACAGCTCTCTGATAGAGCTGCAGGTGCATCGCGGCAATGAAG 360
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DB 361 CACCAAGCTACCTGTCTGGACATTTATTGGACCGTTTACCCCTGCCGGAAGCCCTTGGTGAC 420
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BD195078
LOCUS BD195078 1878 bp DNA linear PAT 17-JUL-2003
DEFINITION Ret ligand (RetL) for stimulating neural and renal growth.
ACCESSION BD195078
VERSION BD195078.1 GI:33004836
KEYWORDS JP 2002515743-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1878)
AUTHORS Nadel,M.S., Hession,C. and Cate,R.L.
TITLE Ret ligand (RetL) for stimulating neural and renal growth
JOURNAL Patent: JP 2002515743-A 9 28-MAY-2002;
COMMENT

COMMENT

OS Unidentified
PN JP 2002515743-A/9
PD 28-MAY-2002
PF 07-MAY-1997 JP 1997542431
PR 08-MAY-1996 US 60/017427, 07-JUN-1996 US 60/019300 PR
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PI MICHELLE SANICOLA NADEL, CATHERINE HESSION, RICHARD L. CATE PC
C07K14/47, C12N15/12, C12Q1/68, A61K48/00, C12N5/10, C12N15/62, PC
C07K16/18,
PC C12N5/06, G01N15/33

CC Strandedness: Single;		
CC Topology: Linear;		
CC Ret ligand (Retl) for stimulating neural and renal growth FH		
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Db	61	CTCTGGAGCCGCGACCTCCACTGCTGATGATCTCTGCTACTGCTGCTGCTGCT 120
Qy	157	GCACCTTGAGCAGGAACTCCCTGCTCCACAGAGAACAGGTTGTGAACAGCTGACCA 216
Db	121	GCACCTTGAGCAGGAACTCCCTTTGCCACAGAGAACAGGTTGTGAACAGCTGACCA 180
Qy	217	GSCCAGAAAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCTACCAAGCACTGGCTC 276
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AR452067 AR452067 1878 bp mRNA linear PAT 20-FEB-2004
LOCUS Sequence 14 from patent US 6677135.
DEFINITION AR452067
ACCESSION AR452067
VERSION AR452067.1 GI:42683406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1878)
AUTHORS Sanicola-Nadel,M., Hession,C., Cate,R.L. and Worley,D.S.
TITLE Ret ligand (RetL) for stimulating neutral and renal growth
JOURNAL Patent: US 6677135-A 14 13-JAN-2004;
Bogen, Inc.: Cambridge, MA
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Query Match 96.5%; Score 1867; DB 6; Length 1878;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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ACCESSION	AR642125.1	GI:62778308	
VERSION	AR642125.1	GI:62778308	
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1878)		
AUTHORS	Sanicola-Nadel,M., Hession,C., Cate,R.L. and Worley,D.S.		
TITLE	Antibodies to Ret and RetL3		
JOURNAL	Patent: US 6861509-A 14 01-MAR-2005;		
	Biogen, Inc.; Cambridge, MA		
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RESULT 13
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LOCUS
DEFINITION
Rattus norvegicus glial cell line derived neurotrophic factor
family receptor alpha 3, mRNA (cDNA clone MGC:94884 IMAGE:7110848),
complete cds.
ACCESSION
BC079378
VERSION
BC079378.1 GI:50927778
KEYWORDS
MGC.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 2070)

REFERENCE
AUTHORS
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2070)

CONSRM
TITLE
NIH MGC Project
Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: TRAK Plate; 182 Row; c Column; 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
Location/Qualifiers

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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 0;
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DEFINITION Mus musculus glial cell line-derived neurotrophic factor family receptor alpha-3 (gfra3) mRNA, complete cds.
ACCESSION AF041842
VERSION AF041842.1 GI:2921578
KEYWORDS SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1244)
AUTHORS Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and Olson, L.
TITLE GFalpha-3, a protein related to GFalpha-1, is expressed in developing peripheral neurons and ensheathing cells
JOURNAL Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
PUBMED 9749804
REFERENCE 2 (bases 1 to 1244)
AUTHORS Tomac, A., Hoffer, B. and Olson, L.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1998) Neuroscience, Karolinska Institute, Doktorsringen 12, Stockholm 17171, Sweden
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ORIGIN

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Job time : 9939 secs

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Db	1200	TCTTTCTCCATCTTCCCTTGAATTTCTGCTGAGACCCCTCTGCTAG	1244

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:57:33 ; Search time 7953 Seconds

(without alignments)
11383.504 Million cell updates/sec

Title: US-10-621-855-4

Perfect score: 1935

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Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gsa1:*

10: gb_gsa2:*

11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1871.8	96.7	1919	4	AK046542 Mus muscu
2	915.6	47.3	1812	4	CR618834 full-leng
3	824	42.6	1112	11	DQ039349 Homo sapi
4	814.8	42.1	880	6	CF585129 AGENCOURT
5	745.8	38.5	958	6	CF585128 AGENCOURT
6	722.8	37.4	740	7	CK782042 UI-M-HJO-
7	633.8	32.8	667	2	BB323153 BB323153
8	603.2	31.2	973	5	EX404447 EX404447
9	598.4	30.9	600	3	BI987608 3203-65 M
10	582.4	30.1	937	5	BQ716490 AGENCOURT
11	569.8	29.4	1054	1	AL558255 AL558255
12	556.2	28.7	589	3	BP771344 BP771344
13	552.6	28.6	958	5	BX329151 BX329151
14	551.2	28.5	992	5	BX375148 BX375148
15	544.8	28.2	634	2	BB645236 BB645236
16	541.2	28.0	1060	1	AL530853 AL530853
17	516.2	26.7	815	3	BI834990 60308882
18	505	26.1	516	2	BF471500 UI-M-BH3-
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25	461.6	23.9	715	7	CN278586 170006001
26	452.6	23.4	499	6	CB712227 AMGNNUC:M
27	447.6	23.1	1138	3	BM546331 AGENCOURT
28	438.2	22.6	460	10	CG483033 OST16426
29	438	22.6	853	11	DQ039350 Pan trogl
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37	413.6	21.4	473	2	BB833560 BB833560
38	408.8	21.1	437	3	BI676681 1c52d09.x
39	396	20.5	445	2	BB830713 BB830713
40	393.6	20.3	875	5	BQ881951 AGENCOURT
41	385.4	19.9	387	8	W99197 mf59f10.r1
42	381.2	19.7	933	5	BQ718109 AGENCOURT
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44	369.2	19.1	405	5	BY378274 BY378274
45	366.8	19.0	398	5	BY027270 BY027270

ALIGNMENTS

RESULT 1	AK046542	AK046542	1919 bp	mrna	linear	HTC 03-APR-2004
LOCUS						
DEFINITION						Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:B330033018 product:glial cell line derived neurotrophic factor family receptor alpha 3, full insert sequence.
ACCESSION						AK046542
VERSION						AK046542.1 GI:26338184
KEYWORDS						HTC; CAP trapper.
SOURCE						Mus musculus (house mouse)
ORGANISM						Mus musculus
REFERENCE						1
AUTHORS						Carninci,P. and Hayashizaki,Y.
TITLE						High-efficiency full-length cDNA cloning
JOURNAL						Meth. Enzymol. 303, 19-44 (1999)
PUBMED						10349636
REFERENCE						2
AUTHORS						Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE						Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL						Genome Res. 10 (10), 1617-1630 (2000)
PUBMED						11042159
REFERENCE						3
AUTHORS						Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Iizawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE						RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL						Genome Res. 10 (11), 1757-1771 (2000)
PUBMED						11076861
REFERENCE						4
AUTHORS						The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE						Functional annotation of a full-length mouse cDNA collection
JOURNAL						Nature 409, 585-590 (2001)
PUBMED						11076861
REFERENCE						5
AUTHORS						The FANTOM Consortium and the RIKEN Genome Exploration Research

Db	718	CCATGTGCCCCCAACGACCGGGGTGCGGGAGCGCGGCGCAACCATCGCCCCCAAC	777
Qy	794	TGGCCCTGCTTCTGTAAACCCCAATTGCTGTGATCTGCGGAGCTTCTCCGTGGGAC	853
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Qy	914	GGGACTTGTGAACTGAGCAGTGCAGATGTCTGCGGGCATACCTGGGGCTGATTTGGGACT	973
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DEFINITION	DQ039349	1112 bp	DNA
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ACCESSION	DQ039349		
VERSION	DQ039349.1	GI:66890558	
KEYWORDS	GSS.		
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1112)		
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,		
	Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,		
	White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and		
	Chimpanzees		
JOURNAL	(ex) PLOS Biol. 3 (6), E170 (2005)		
PUBMED	15869325		
REFERENCE	2 (bases 1 to 1112)		
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,		
	Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,		
	White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,		
	Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering		
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Matches 932;	Conservative 0;	Mismatches 180;	Indels 0; Gaps 0;
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Qy	291	TAGCAGGCCGCTGCCCTTAGAGAGTGTGCATGTCTGCAGACTGCTTAGAGGCACAG	350
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Qy	351	AACAACTCAGGAACAGCTCTCTGTAGACTGCAGGTGCCATCGCGCGCATGAAGCACCAAG	410
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Qy	411	CTACTGCTCGCAATTTATTGGACCGTTACCCCTGCCGAGGCTTGGTGAACCTACGAGT	470
Db	241	TTGCTGCTGGCAATCTATTGGACCGTTACCGTGGCCGAGGCTTGGTAACCTATGAGC	300

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QY 531 AGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTATGCTGTACTC 590
Db 361 AACTGAACATGCTCAAAACAGACTCAGACCTCTGCTCAAGTTTGCATGCTGTGTACTC 420
QY 591 TTCAACGACAAGTGTGACCCCTCGCGAAGGCTTACGGGAGGATGCTCAGGGATCCGCT 650
Db 421 TCAATGACAAGTGTGACCCCTCGCGAAGGCTTACGGGAGGATGCTCAGGGATCCGCT 480
QY 651 GCCAGGCCACTCTGCTTACGCCCTAGCCAGCTGCGCTCTCTTTTGAAGAGGACAGATGCC 710
Db 481 GCCAGGCCACTCTGCTTACGCCCTAGCCAGCTGCTCACTTTCTTGAAGAGGCGCGGAGCC 540
QY 711 AGCTCAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
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Db 961 TTCACAGGCACTCTTCTCCAGGAGTGGGAGAGTCTACTTTTTCAGTGGTGAGGAGC 1020
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RESULT 4
CF585129/c
LOCUS CF585129 880 bp mRNA linear EST 24-SEP-2003
DEFINITION AGENCOURT 8845811 updated NIH_MGC_137 Mus musculus cDNA clone
IMAGE:6430904 3', mRNA sequence.
ACCESSION CF585129
VERSION CF585129.1 GI:35198391
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 880)
REFERENCE NIH-MGC http://mgc.mci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
```

JOURNAL
COMMENT

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>

Plate: IRBD10 row: g column: 09
High quality sequence stop: 585.

FEATURES
source

Location/Qualifiers
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/lab_host="DH10B"
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/note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI;
Site 2: NotI; Library consists of a pool of clones
rearranged from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-NMS1, Amplified Melton mouse
islets 1 M1S1-A, and Kaestner ngn3 wt. Clones rearranged in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.1%; Score 814.8; DB 6; Length 880;
Best Local Similarity 96.0%; Pred. No. 4e-204;
Matches 846; Conservative 0; Mismatches 33; Indels 2; Gaps 1;

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10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayaishizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayaishizaki, Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

source

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1. 667
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/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTAAATTAATATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

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ORIGIN

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Matches 652; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

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Qy 1304 TGTCCTCTCCACACACCCAGACTGATTTGCAGCCTGTGTGGGGAGAGAACTCGCCAGCC 1363
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Qy 1364 TGTGAAGAAGACGAGCGGTGTACACAGCAACCCGGAACCCACAGGATTCGCGACA 1423
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Qy 1424 CATCCCTCTGCTCCAGAGAGGCTCTAGAGTGAGGGCTGTGACCTTCGATCCTCAG 1483
Db 181 CATCCCGTCTGCTCCNNAAGAGGCTCTAGAGTGAGGGCTGTGACCTTCGATCCTCAG 240

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Db 421 TCTCAGAGAGGAGGCTTAAGGTTCTGAGTGATGAGAAAATGTTCTTGTGTGG 480
Qy 1724 AAGGCTGTGCTCCAGGCTCCACGCTCCCTCTGAATGAAGATAAAACCTGCTGTGTCT 1783
Db 481 AAGGCTGTGCTCCAGGCTCCACGCTCCCTCTGAATGAAGATAAAACCTGCTGTGTCT 540
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Db 541 TGACTGTCTTGCCAGGCAATCTGAACATTTGGGCTGAAGAGCTAAAGTCTTTGGGTCT 600
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Db 661 TTGACTT 667

RESULT 8
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CL0BB029ZH02 5-PRIME, mRNA sequence.
ACCESSION BX404447
VERSION BX404447.2 GI:46924437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 973)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30635183.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3046.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CL0BB029ZH02RPI&c=3046.r.
Location/Qualifiers
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector."

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FEATURES

source


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Db      541 AGAGCGGGGTAAACACCATCGCCCCAGTTGGCGCCTGCTCTGTGTAAACCCCAATTGCC 600

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IMAGE:6194172 5', mRNA sequence.
ACCESSION BQ716490
VERSION   BQ716490.1 GI:21855387
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
1 (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.illnl.gov
Plate: LAM13598 row: p column: 13
High quality sequence stop: 653.
Location/Qualifiers
1. 937
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Note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
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Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTGATTCAGATCGCGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN
Query Match 30.1%; Score 582.4; DB 5; Length 937;
Best Local Similarity 84.0%; Pred. No. 1.5e-142;
Matches 569; Conservative 0; Mismatches 126; Indels 1; Gaps 1;

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QY      274 CTCCTGCACCTCCAGTTTAAGCAGCGCGCTGCTTAGGAGTCTGCATGCTGCGAGA 333
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QY      394 GCGCATGAAGCAACCAAGCTACTGCTGTGGAATTTATTTGACCGTTACCTGCCCGGAG 453
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LOCUS   AL558255
DEFINITION AL558255 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
          Homo sapiens cDNA clone CS0DU001YA19 5-PRIME, mRNA sequence.
ACCESSION AL558255
VERSION   AL558255.3 GI:46183654
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
1 (bases 1 to 1054)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31280054.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3046.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DU001YA100P1&c=3046.r.
Location/Qualifiers
FEATURES
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RESULT 12			
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LOCUS			
DEFINITION			
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VERSION	BP771344.1	GI:50230042	
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
COMMENT			
FEATURES			
source			
origin			
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Best Local Similarity	99.5%	Pred. No. 1.1e-135	
Matches	558	Conservative 0	Mismatches 3
		Indels 0	Gaps 0
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Qy	1432	CTGCTCCAGAAAGAGGTCTTAGAACTGAGGGCTGTGACCCCTTC	149
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Qy	1492	TTTCAAAACCTCCCTTGCCTTCCTTCTGGCTCAGGCTGCTCCTCT	155
Db	468	TTTCAAAACCTCCCTTGCCTTCCTTCTGGCTCAGGCTGCTCCTCT	409
Qy	1552	TGGGTCCAGTTTGGCCCTCTGTTCTGATGGGATTTAGGGCTCACCT	161
Db	408	TGGGTCCAGTTTGGCCCTCTGTTCTGATGGGATTTAGGGCTCACCT	349
Qy	1612	CTGTTTCCAGGACCAACAGAGGCTAAGGAATCAGTCAATTCCTGTT	167
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/lab_host="DH10B"
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gland"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGAGCTTTTTTTTTTTTTTTN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAATATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:
BamHI"
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ORIGIN

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Query Match      28.2%; Score 544.8; DB 2; Length 634;
Best Local Similarity 96.2%; Pred. No. 1.2e-132;
Matches 558; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:37:03 ; Search time 1191 Seconds
(without alignments)
10828.027 Million cell updates/sec

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Perfect score: 1935
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
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- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1935	100.0	1935	3	Aaz29100	Aaz29100 Murine Gf
2	1897	97.5	1889	2	Aav00249	Aav00249 Mouse Ret
3	1887	97.5	1889	12	ADJ58708	ADJ58708 Murine re
4	1887	97.5	1889	14	ADY53844	ADY53844 Mouse ret
5	1887	97.5	1889	14	ADZ00208	ADZ00208 Mouse Ret
6	1867	96.5	1878	2	AAV00256	AAV00256 Mouse Ret
7	1867	96.5	1878	12	ADJ58706	ADJ58706 Murine re
8	1867	96.5	1878	14	ADY53842	ADY53842 Partial m
9	1867	96.5	1878	14	ADZ00206	ADZ00206 Mouse Ret
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11	955.2	49.4	1878	2	AAV99334	AAV99334 Glial cel
12	934.6	48.3	1829	3	AAZ93702	AAZ93702 PRO538 DN
13	934.6	48.3	1829	3	AAA88519	AAA88519 Human PRO
14	934.6	48.3	1829	3	AAA77617	AAA77617 Human PRO
15	934.6	48.3	1829	3	AAA54101	AAA54101 PRO538 cD
16	934.6	48.3	1829	13	ADT94301	ADT94301 Human PRO
17	934.4	48.3	1792	3	AAZ29104	AAZ29104 Human GFR
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19	928.2	48.0	1829	3	AAZ58234	AAZ58234 Human PRO

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25	854.4	44.2	1203	14	ADV42887	ADV42887 Human psy
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42	103.4	5.3	521	13	ACF84889	ACF84889 Human SIR
43	102	5.3	1392	3	AAZ91456	AAZ91456 Human neu
44	102	5.3	1392	6	ABN87349	ABN87349 Human neu
45	102	5.3	1392	6	ABK50453	ABK50453 Human neu

ALIGNMENTS

RESULT 1

AAZ29100

ID AAZ29100 standard; cDNA; 1935 BP.

XX AC AAZ29100;

XX DT 07-FEB-2000 (first entry)

XX DE Murine GFRalpha3 cDNA.

XX KW Murine GFRalpha3; GFRalpha3; GFRalpha1;

glial-cell-line-derived neurotrophic factor family receptor alpha-3;
probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
cell proliferation; cell differentiation; GFRalpha3-containing cell;
Ret-containing cell; peripheral nervous system disease; diabetes;
human immunodeficiency virus; chemotherapeutic agent treatment;
autonomic nervous system dysfunction; transgenic animal; ds.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX CDS 89..1282

FT sig_peptide /tag= a

FT /product= "Murine GFRalpha 3"

FT /tag= b

XX PN WO9949039-A2.

XX PD 30-SEP-1999.

XX PF 19-MAR-1999; 99WO-US006098.

XX PR 23-MAR-1998; 98US-0079124P.

XX PR 13-APR-1998; 98US-0081569P.

XX (GETH) GENENTECH INC.

XX PI De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;

XX DR WPI; 2000-038358/03.

XX DR P-PSDB; AAY15174.

XX PT New isolated GPR-alpha3 nucleic acid, used to develop products for
PT treating diseases or conditions involving peripheral nervous system or
PT autonomic nervous system.
XX Example 1; Fig 1; 112pp; English.
XX The present sequence encodes full length mouse glial-cell-line-derived
CC neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
CC sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be
CC used as a probe to screen for homologous DNA. GFRalpha3 possess neuronal
CC cell activation property. GFRalpha3 ligands can be used to stimulate
CC proliferation, growth, survival, differentiation, metabolism or
CC regeneration of GFRalpha3- and Ret-containing cells. They can be useful
CC in the treatment of peripheral nervous system diseases, eg. those
CC associated with diabetes, human immunodeficiency virus, or
CC chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
CC can be used to treat autonomic nervous system dysfunctions. The products
CC can also be used for detection, diagnosis and production of transgenic
CC animals
XX Sequence 1935 BP; 418 A; 584 C; 490 G; 443 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 1935; DB 3; Length 1935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 829 TCTGCGGAGCTTCTGCGTGGGAGCCCTTTGTGACAGATCAGCCCTGATGGACTTCCAGAC 888
Db 781 TCTGCGGAGCTTCTGCGTGGGAGCCCTTTGTGACAGATCAGCCCTGATGGACTTCCAGAC 840
QY 889 CCACCTGTATCTATGACATCCTTTGGGACTTGTGGAATTTGCAACTGAGCAGTCCAGATGTCTCG 948
Db 841 CCACCTGTATCTATGACATCCTTTGGGACTTGTGGAATTTGCAACTGAGCAGTCCAGATGTCTCG 900
QY 949 GGCATACCTGGGGCTGTATGGGACTGCGCATGACCCCAAACTTCATCAGCAGGTCAACAC 1008
Db 901 GGCATACCTGGGGCTGTATGGGACTGCGCATGACCCCAAACTTCATCAGCAGGTCAACAC 960
QY 1009 TACTGTTCCTTAAAGCTGACCTGCGAGGAGCGGCAACCTTACAGGACGAGTGTGAACA 1068
Db 961 TACTGTTCCTTAAAGCTGACCTGCGAGGAGCGGCAACCTTACAGGACGAGTGTGAACA 1020
QY 1069 GCTGAAAGGCTCTTCTCTCCAGAACCCCTCGCTCGTGGAGGCCATTTGAGCTAAGATCGG 1128
Db 1021 GCTGAAAGGCTCTTCTCTCCAGAACCCCTCGCTCGTGGAGGCCATTTGAGCTAAGATCGG 1080
QY 1129 TTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTTCAAGTGTGACAGA 1188
Db 1081 TTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTTCAAGTGTGACAGA 1140
QY 1189 GCAGAACAGCACCTCTCTGAGACTGCGCCAGGCTTACCAATTTCTTTCTTCTCCAT 1248
Db 1141 GCAGAACAGCACCTCTCTGAGACTGCGCCAGGCTTACCAATTTCTTTCTTCTCCAT 1200
```

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QY 1249 CTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAGGGTCTCTTTGTCC 1308
Db 1201 CTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAGGGTCTCTTTGTCC 1260
QY 1309 TCTCCACACACCCAGACTGATTTTGCAGCCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1368
Db 1261 TCTCCACACACCCAGACTGATTTTGCAGCCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1320
QY 1369 AAGAAGACGCAAGCCTGTCTACACAGCAACCCGGAAACCAACCAAGGCAATTCGCGAGCACTCC 1428
Db 1321 AAGAAGACGCAAGCCTGTCTACACAGCAACCCGGAAACCAACCAAGGCAATTCGCGAGCACTCC 1380
QY 1429 GCTGTCTCCAGAGAGGCTCTTAGAGTGAAGGCTGTGACCCCTTCCGATCTCTAGCGGCT 1488
Db 1381 GCTGTCTCCAGAGAGGCTCTTAGAGTGAAGGCTGTGACCCCTTCCGATCTCTAGCGGCT 1440
QY 1489 AGTTTCAAACCTCCCTTGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
Db 1441 AGTTTCAAACCTCCCTTGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1549 TTGTGGGTCCAAGTTTGGCTTCTCTCTGATTTGATTTAGCGGCTCACCTCCAGCGCTTC 1608
Db 1501 TTGTGGGTCCAAGTTTGGCTTCTCTCTGATTTGATTTAGCGGCTCACCTCCAGCGCTTC 1560
QY 1609 TTCTGTCTCCAGAGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTGCTGCTGCTTCTCC 1668
Db 1561 TTCTGTCTCCAGAGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTGCTGCTGCTTCTCC 1620
QY 1669 AGGAAGCAGGCTAAGGGTCTGAGGTGACCTGAGAAATAATGTTTCTTGTGTGGAGGC 1728
Db 1621 AGGAAGCAGGCTAAGGGTCTGAGGTGACCTGAGAAATAATGTTTCTTGTGTGGAGGC 1680
QY 1729 TGGTGTCTCCAGCTTCCAGCTCTCTGAATTTGAAAGATAAAACCTGCTGCTGCTTGAAT 1788
Db 1681 TGGTGTCTCCAGCTTCCAGCTCTCTGAATTTGAAAGATAAAACCTGCTGCTGCTTGAAT 1740
QY 1789 GCTGTGCGAGCAATCTGAAACATTTGGGCAATGAAGAGCTAAAGTCTTTGGGTCTTGTGTT 1848
Db 1741 GCTGTGCGAGCAATCTGAAACATTTGGGCAATGAAGAGCTAAAGTCTTTGGGTCTTGTGTT 1800
QY 1849 AACTCTTATTTACTCTCCCAATTTCCCTAGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1908
Db 1801 AACTCTTATTTACTCTCCCAATTTCCCTAGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 4
ADY53844
ID ADY53844 standard; cDNA; 1889 BP.
XX
AC ADY53844;
XX
DT 05-MAY-2005 (first entry)
XX
DE Mouse retL3 cDNA.
XX
KW DNA purification; immune stimulation; ret ligand; gene; ss.
XX
OS Mus sp.
XX
PN US6861509-B1.
XX
PD 01-MAR-2005.
XX
PF 21-JAN-2000; 2000US-00489407.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
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QY 769 GGGGGTAACACCATCGCCCGCCAGTTGGCCCTGCTCTGTAAACCCCAATTTGCTTGA 828
DB 721 GGGGGTAACACCATCGCCCGCCAGTTGGCCCTGCTCTGTAAACCCCAATTTGCTTGA 780
QY 829 TCTGGGAGCTTCTCGCGTGGGAGCCCTTTGTGACAGATCAGCCCTGTAGTGGACTTCCAGAC 888
DB 781 TCTGGGAGCTTCTCGCGTGGGAGCCCTTTGTGACAGATCAGCCCTGTAGTGGACTTCCAGAC 840
QY 889 CAACGTCTCATCTATGAGACATCTTGGGACATTTGTGCAACTGTGCAAGTCCAGATGTCTGG 948
DB 841 CCACTGTCTCATCTATGAGACATCTTGGGACATTTGTGCAACTGTGCAAGTCCAGATGTCTGG 900
QY 949 GGCATACCTTGGGGCTGATTTGGGACATGCGATGACCCCAAACTTTCATCAGCAAGTCAACAC 1008
DB 901 GGCATACCTTGGGGCTGATTTGGGACATGCGATGACCCCAAACTTTCATCAGCAAGTCAACAC 960
QY 1009 TACTGTTGCTTTAAGCTGACCTGCGGAGCGAGCGCAACTTACAGGACGAGTGTGAACA 1068
DB 961 TACTGTTGCTTTAAGCTGACCTGCGGAGCGAGCGCAACTTACAGGACGAGTGTGAACA 1020
QY 1069 GCTGAAAGGCTCTTCTCCAGAACCCCTGCTCTGTGAGGCGCAATTCAGCTTAAGATGG 1128
DB 1021 GCTGAAAGGCTCTTCTCCAGAACCCCTGCTCTGTGAGGCGCAATTCAGCTTAAGATGG 1080
QY 1129 TTTCCACAGACAGCTCTTCTCCAGAACCTGGGACAGCTCTACTTTTTCAGTGGTGCAGCA 1188
DB 1081 TTTCCACAGACAGCTCTTCTCCAGAACCTGGGACAGCTCTACTTTTTCAGTGGTGCAGCA 1140
QY 1189 GCAGAACAGCAACCTGCTCTGAGACTGCGAGCCAGGCTACCCATTCCTTTCTTCCTCAT 1248
DB 1141 GCAGAACAGCAACCTGCTCTGAGACTGCGAGCCAGGCTACCCATTCCTTTCTTCCTCAT 1200
QY 1249 CCTTCCCTTGATCTGTGTCAGACCTCTGTGAGCTGGGCTTCCTCAGGCTCCTTTGTCC 1308
DB 1201 CCTTCCCTTGATCTGTGTCAGACCTCTGTGAGCTGGGCTTCCTCAGGCTCCTTTGTCC 1260
QY 1309 TCTCCACACACCCAGACTGATTTTCAGCCTGTGTGGGAGAGAACTCGCCAGCCCTGTGG 1368
DB 1261 TCTCCACACACCCAGACTGATTTTCAGCCTGTGTGGGAGAGAACTCGCCAGCCCTGTGG 1320
QY 1369 AAGAAAGCGCAGCTGTCTACAGCAACCCGGAACCAACAGGCAATTCGCGACGACATCC 1428
DB 1321 AAGAAAGCGCAGCTGTCTACAGCAACCCGGAACCAACAGGCAATTCGCGACGACATCC 1380
QY 1429 CGTCTGCTCCAGAGAGGCTTTAGAGTGAAGGCTGTGACCTTCGATTCGATTCGAGCGGT 1488
DB 1381 CGTCTGCTCCAGAGAGGCTTTAGAGTGAAGGCTGTGACCTTCGATTCGATTCGAGCGGT 1440
QY 1489 AGTTTTCACCACTCCCTTGGCCCTGCTTCTGCTGAGGCTGCTCTCTCTCTAGGACT 1548
DB 1441 AGTTTTCACCACTCCCTTGGCCCTGCTTCTGCTGAGGCTGCTCTCTCTCTAGGACT 1500
QY 1549 TTGTGGGCTCCAGTTTTCCTTCTGTGATGGTGTAGTGGGCTCACCTCCAGCGCTTC 1608
DB 1501 TTGTGGGCTCCAGTTTTCCTTCTGTGATGGTGTAGTGGGCTCACCTCCAGCGCTTC 1560
QY 1609 TTCCTGTTTCCAGACACCCAGAGGCTAAGGAATCAGTTCATTCCTGTGCTTCCTTCCTCC 1668
DB 1561 TTCCTGTTTCCAGACACCCAGAGGCTAAGGAATCAGTTCATTCCTGTGCTTCCTTCCTCC 1620
QY 1669 AGGAAGGCGCAGGCTAAGGGTTCAGGTGACTCAGAAATAATGTTTCTTTGTGTGAAGGC 1728
DB 1621 AGGAAGGCGCAGGCTAAGGGTTCAGGTGACTCAGAAATAATGTTTCTTTGTGTGAAGGC 1680
QY 1729 TGGTGTCTCCAGCTCCAGCTCCCTCTGAATGGAAGATAAAACCTGCTGGTGTCTTGACT 1788
DB 1681 TGGTGTCTCCAGCTCCAGCTCCCTCTGAATGGAAGATAAAACCTGCTGGTGTCTTGACT 1740
QY 1789 GCTTGTCCAGGCAATCTTGAAATTTGGGCTAAGAGCTAAGCTTTGGTCTTGTTT 1848
DB 1741 GCTTGTCCAGGCAATCTTGAAATTTGGGCTAAGAGCTAAGCTTTGGTCTTGTTT 1800

QY 1849 AACTCTATTACTGTCCCAAAATTCCTAGTCCCTGGGTTCATGATTAAACATTTTGAC 1908
DB 1801 AACTCTATTACTGTCCCAAAATTCCTAGTCCCTGGGTTCATGATTAAACATTTTGAC 1860
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935
DB 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887
RESULT 6
AAV00256
ID AAV00256 standard; cDNA; 1878 BP.
XX
AC AAV00256;
XX
DT 21-MAY-1998 (first entry)
XX
Mouse Ret ligand retL3 cDNA partial clone (EST AA50083).
XX
Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
XX
cell growth; renal cell; nerve cell; renal failure; nephritis;
XX
kidney transplant; toxic injury; hypoxic injury; infection; meningitis;
XX
motor neuron disease; multiple sclerosis; infection; meningitis;
XX
myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
XX
spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
XX
muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
XX
Mus musculus.
XX
Key Location/Qualifiers
FH CDS 205..1245
FT /*tag= a
XX
WO9744356-A2.
XX
27-NOV-1997.
XX
07-MAY-1997; 97WO-US007726.
XX
08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 11-APR-1997; 97US-0043533P.
XX
(BIOJ) BIOGEN INC.
XX
Sanicola-Nadel M, Hession C, Cate RL;
XX
WPI; 1998-018431/02.
DR P-PSDB; AAW37465.
XX
New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
and improving survival of injured cells, especially renal or nerve cells.
XX
Disclosure; Page 71-73; 113pp; English.
XX
This sequence comprises EST AA050083, identified as a partial cDNA for
CC mouse Ret ligand (RetL) RetL3 (see AAW37465), by screening of an EST
CC database with rat RetL1 (see AAW37457). A full-length mouse retL3 cDNA
CC clone (see AAV00249) was obtained by combining AA050083 with a clone
CC obtained by 5'RACE. Rat, mouse and human retL1, retL2 and retL3 cDNA
CC sequences (see AAV00245-51) and encoded polypeptides (see AAW37457-63)
CC are claimed and can be used in methods for promoting cell growth and
CC improving survival of cells, especially renal or neural cells
XX
Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T; 0 U; 0 Other;
SQ
Query Match 96.5%; Score 1867; DB 2; Length 1878;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 37 CGCGCGCCCGCAGCGCAGAGAGCGCTGTGCGATCCCGGGCGTCCACCGCCATGGGGCT 96

[illegible]

Db	1080	AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCCAAGGACTGGGACAGACTCTACTATTTTTC	11139
Qy	1177	AGTGGTGCAGCAGCAGAAACAGCAACCTGCTCTGAGACTGCAGCCAGGCTACCCCAATTC	12336
Db	1140	AGTGGTGCAGCAGCAGAAACAGCAACCTGCTCTGAGACTGCAGCCAGGCTACCCCAATTC	11199
Qy	1237	TTCTTTTCTCCATCCTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAG	12996
Db	1200	TTCTTTTCTCCATCCTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAG	12559
Qy	1297	GGTCCCTTGTCTCTCCACACACCCAGACTGATTTTGACGCTGTGGTGGGAGAGAACTC	13556
Db	1260	GGTCCCTTGTCTCTCCACACACCCAGACTGATTTTGACGCTGTGGTGGGAGAGAACTC	13119
Qy	1357	GCCAGCCTGTGGAGAGACGACGCTGTCTACACAGCAACCCGAAACCAACCAAGGCATTC	14116
Db	1320	GCCAGCCTGTGGAGAGACGACGCTGTCTACACAGCAACCCGAAACCAACCAAGGCATTC	13779
Qy	1417	CGCAGCACATCCCGTCTGTCTCCAGAGAGAGTCTTAGAAGTAGGGGCTGTGACCCCTTCCGA	14776
Db	1380	CGCAGCACATCCCGTCTGTCTCCAGAGAGAGTCTTAGAAGTAGGGGCTGTGACCCCTTCCGA	14339
Qy	1477	TCCTGAGCGGCTAGTTTTCAAACCTCCCTTGGCCCTGCTTCTTCTGGCTCAGGCTGCTC	15336
Db	1440	TCCTGAGCGGCTAGTTTTCAAACCTCCCTTGGCCCTGCTTCTTCTGGCTCAGGCTGCTC	14999
Qy	1537	CTCCTTAGGACTTTGTGGGTCCAGTTTGTGCTTCTGTTCTGTAGTGGTGAATTAGCGGCTCAC	15996
Db	1500	CTCCTTAGGACTTTGTGGGTCCAGTTTGTGCTTCTGTTCTGTAGTGGTGAATTAGCGGCTCAC	15559
Qy	1597	CTCAGCGGCTTCTTCTGTTTTCCAGGACACACCCAGAGGCTAAGGAATCAGTCAATTCCTT	16556
Db	1560	CTCAGCGGCTTCTTCTGTTTTCCAGGACACACCCAGAGGCTAAGGAATCAGTCAATTCCTT	16119
Qy	1657	GTTGCTTCTCCAGGAGGCGAGGCTAAGGGTCTGTGAGGTGACCTGAGAAAATGTTTCCCTT	17116
Db	1620	GTTGCTTCTCCAGGAGGCGAGGCTAAGGGTCTGTGAGGTGACCTGAGAAAATGTTTCCCTT	16779
Qy	1717	TGTGTGGAAGGCTGGTGCTCCAGCTCCAGTCCCTCTGAATGGAAGATAAAAACCTGCT	17776
Db	1680	TGTGTGGAAGGCTGGTGCTCCAGCTCCAGTCCCTCTGAATGGAAGATAAAAACCTGCT	17339
Qy	1777	GGTGTCTTGACTGCTCTGCGAGCAATCTCTGAACATTTGGGCAATGAAGAGCTAAAGTCTT	18336
Db	1740	GGTGTCTTGACTGCTCTGCGAGCAATCTCTGAACATTTGGGCAATGAAGAGCTAAAGTCTT	17999
Qy	1837	TGGGTCTTGTTTAACTCTCTTAATTACTGTCCCAAAATTCCTTCTGGGTCATGATTT	18996
Db	1800	TGGGTCTTGTTTAACTCTCTTAATTACTGTCCCAAAATTCCTTCTGGGTCATGATTT	18559
Qy	1897	AAACATTTTGACTTAAAAA 1915	
Db	1860	AAACATTTTGACTTAAAAA 1878	

RESULT 7
ADT58706

ADJ58706
ID ADJ58706 standard; cDNA; 1878 BP.

XX
AC ADJ58706:XX
DT 06-MAY-2004 (first entry)

XX DE Murine retL3 partial cDNA.

XX	Tissue growth; retL protein; organ failure; foetal malformation;
XX	tumour growth; renal tissue; cytostatic; vulnery; nephrotropic;
KW	gene; ss.
KW	

XX	Mus sp
SO	

XX	Key	Location/Qualifiers
FH	CDS	205. .1245
FT		

QY 1477 TCGTAGGGCTAGTTTCAAACTCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTC 1536
DB 1440 TCGTAGGGCTAGTTTCAAACTCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTC 1499
QY 1537 CTCCTTAGGACTTTGGGCTCAGTTTGGCTTCTGTTCTGATGCTGATTTAGCGCTCAC 1596
DB 1500 CTCCTTAGGACTTTGGGCTCAGTTTGGCTTCTGTTCTGATGCTGATTTAGCGCTCAC 1559
QY 1597 CTCACAGCGCTTCTTCTGTTTCCAGGACCCAGAGCTAAGGAATCAGTTCCTT 1656
DB 1560 CTCACAGCGCTTCTTCTGTTTCCAGGACCCAGAGCTAAGGAATCAGTTCCTT 1619
QY 1657 GTTGCTTCTCAGGAGCGCTAAGGTTCTGAGGTGACTGAGAAAATGTTTCTT 1716
DB 1620 GTTGCTTCTCAGGAGCGCTAAGGTTCTGAGGTGACTGAGAAAATGTTTCTT 1679
QY 1717 TGTGTGGAAGGCTGCTGCTCCAGGCTCCAGCTCCCTCTGAAATGGAAGATAAAACCTGCT 1776
DB 1680 TGTGTGGAAGGCTGCTGCTCCAGGCTCCAGCTCCCTCTGAAATGGAAGATAAAACCTGCT 1739
QY 1777 GGTGCTTCTGACTGCTGCTGCGAGGCAATCCTGAACATTTTGGGCATGAAGAGCTTAAAGTCTT 1836
DB 1740 GGTGCTTCTGACTGCTGCTGCGAGGCAATCCTGAACATTTTGGGCATGAAGAGCTTAAAGTCTT 1799
QY 1837 TGGGTCTTGTAACTTCTTACTGTGCTCCCAAAATCCCTAGTCCCTTGGTCAATGAT 1896
DB 1800 TGGGTCTTGTAACTTCTTACTGTGCTCCCAAAATCCCTAGTCCCTTGGTCAATGAT 1859
QY 1897 AAACATTTTGACTTAAAA 1915
DB 1860 AAACATTTTGACTTAAAA 1878

RESULT 8

ADY53842

ID ADY53842 standard; cDNA; 1878 BP.

XX AC

XX ADY53842;

XX DT 05-MAY-2005 (first entry)

XX DE Partial mouse retL3 cDNA.

XX KW DNA purification; immune stimulation; ret ligand; gene; ss.

XX OS Mus sp.

XX PN US6861509-B1.

XX PD 01-MAR-2005.

XX PF 21-JAN-2000; 2000US-00489407.

XX PR 08-MAY-1996; 96US-0017427P.

XX PR 07-JUN-1996; 96US-0019300P.

XX PR 16-JUL-1996; 96US-0021859P.

XX PR 23-AUG-1996; 96US-0023444P.

XX PR 11-APR-1997; 97US-0043533P.

XX PR 07-MAY-1997; 97MO-US007726.

XX PR 06-NOV-1998; 98US-00187906.

XX PA (BIOJ) BIOGEN INC.

XX PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;

XX DR WPI; 2005-201184/21.

XX DR P-PSDB; ADY53843.

XX PT New anti-ret ligand (RetL) antibody, useful for treating acute renal

XX PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as

XX PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.

XX PS Disclosure; SEQ ID NO 14; 66pp; English.

XX

CC

CC

CC

CC

XX

SQ

The invention relates to an antibody produced by a hybridoma selected from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to stimulate neural and renal cell growth. This sequence corresponds to a nucleic acid sequence of the rat retL1 cDNA of the invention.

Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T; 0 U; 0 Other;

Query Match 96.5%; Score 1867; DB 14; Length 1878;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 37 CGCGGCGCCAGCGGACGAGCGCTGTCGATCCCGGGGCTCCACCGGCATGGGGCT 96

DB 1 CGCGGCGCCAGCGGACGAGCGCTGTCGATCCCGGGGCTCCACCGGCATGGGGCT 60

QY 97 CTCTCGAGCGCCGCGACCTCCACATGCTGCTACTGCTGCTGCTGCTGCTGCTGCT 156

DB 61 CTCTCGAGCGCCGCGACCTCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 157 GCCACTTGGAGCAGGAAAATCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACCCA 216

DB 121 GCCACTTGGAGCAGGAAAATCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACCCA 180

QY 217 GGCAGAGAAAGAAATGCCGAGGCTAATCCGCTTGCAGAGCTGCCCTACAGCAGCCTGGGCTC 276

DB 181 GGCAGAGAAAGAAATGCCGAGGCTAATCCGCTTGCAGAGCTGCCCTACAGCAGCCTGGGCTC 240

QY 277 CTGCACCTCCAGTTTAAAGCAGCGCTGCCCTTAGAGGAGTCTGCCATGTCTGCAGACTG 336

DB 241 CTGCACCTCCAG - TTAAGCAGCGCTGCCCTTAGAGGAGTCTGCCATGTCTGCAGACTG 299

QY 337 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAGGTGCCATTCGGCG 396

DB 300 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAGGTGCCATTCGGCG 359

QY 397 CATGAAGCAGCAGCTACCTGTCTGGAATTTATTTGACCCCTTACCCCTGCCGAGGCT 456

DB 360 CATGAAGCAGCAGCTACCTGTCTGGAATTTATTTGACCCCTTACCCCTGCCGAGGCT 419

QY 457 TGGTGACTACGAGTTGGATGTCTCACCTATGAAGACACAGTGACAGCAAAACCTCGAA 516

DB 420 TGGTGACTACGAGTTGGATGTCTCACCTATGAAGACACAGTGACAGCAAAACCTCGAA 479

QY 517 AATGAATCTTAGCAAGTTGAAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAATTCG 576

DB 480 AATGAATCTTAGCAAGTTGAAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAATTCG 539

QY 577 TATGCTGTGACTCTTTCAGGACAAAGTGTGACCGCTTGCAGAGGCTTACGGGAGGCGATG 636

DB 540 TATGCTGTGACTCTTTCAGGACAAAGTGTGACCGCTTGCAGAGGCTTACGGGAGGCGATG 599

QY 637 CTCAGGGATCCGCTGCCAGCGCCACCTCTGCTAGCCAGCTGGCTCTCTTTTGAGAA 696

DB 600 CTCAGGGATCCGCTGCCAGCGCCACCTCTGCTAGCCAGCTGGCTCTCTTTTGAGAA 659

QY 697 GGCAGCAGAGTCCCAAGCTCAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756

DB 660 GGCAGCAGAGTCCCAAGCTCAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719

QY 757 CTGTGGGAGCGGGGCTTAACACATGCCGCCAGTTGCGCCCTCTGTTAAACCCC 816

DB 720 CTGTGGGAGCGGGGCTTAACACATGCCGCCAGTTGCGCCCTCTGTTAAACCCC 779

QY 817 CAATTTGCTGATCTGCGGAGCTTCTGCGGTGGGACCTTTTGTGCAGATCACGCTGAT 876

DB 780 CAATTTGCTGATCTGCGGAGCTTCTGCGGTGGGACCTTTTGTGCAGATCACGCTGAT 839

QY 877 GGCATTTCCAGACCCACATGCTCATCTTATGGACATCTTGGGACTTGTGCACTGACGAGTC 936

DB 840 GGCATTTCCAGACCCACATGCTCATCTTATGGACATCTTGGGACTTGTGCACTGACGAGTC 899

QY 937 CAGATGTCTGCGGGCAATACCTGGGGGCTGATTTGGGACTGCCATGACCCCAAACTTCATCAG 996

Db 900 CAGATGTCTGCGGCATACCTGGGCTGATTGGGACTGCCATGACCCCAAACTTCATCAG 959
Qy 997 CAAAGTCAACACTACTGTTCCTTAAGCTGCACCTGCCGAGCGCAGCACTACAGGA 1056
Db 960 CAAAGTCAACACTACTGTTCCTTAAGCTGCACCTGCCGAGCGCAGCACTACAGGA 1019
Qy 1057 CCAAGTGTGAACAGCTGGAAGGTCTCTTCCAGAACCCCTGCTCGCTCGTGGAGCCATTGC 1116
Db 1020 CCAAGTGTGAACAGCTGGAAGGTCTCTTCCAGAACCCCTGCTCGTGGAGCCATTGC 1079
Qy 1117 AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGAGCTGGGAGACTCTACTTTTC 1176
Db 1080 AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGAGCTGGGAGACTCTACTTTTC 1139
Qy 1177 AGTGTGACGACGACAGACAGCAACCCCTGCTCTGAGACTGCAGCCAGGCTACCCATTCT 1236
Db 1140 AGTGTGACGACGACAGACAGCAACCCCTGCTCTGAGACTGCAGCCAGGCTACCCATTCT 1199
Qy 1237 TTTCTTTCTCCATCCTTCCCTTTCATTTCTGTGCAGACCCCTCTGTTAGCTGGGCTTCTCAG 1296
Db 1200 TTTCTTTCTCCATCCTTCCCTTTCATTTCTGTGCAGACCCCTCTGTTAGCTGGGCTTCTCAG 1259
Qy 1297 GGTCTCTTTCTCTCTCCACACACCCAGACTGATTTGCAGCCTGTGTGGAGAGAACTC 1356
Db 1260 GGTCTCTTTCTCTCTCCACACACCCAGACTGATTTGCAGCCTGTGTGGAGAGAACTC 1319
Qy 1357 GCCACCTGTGGAAGACGACGCGTGTACACAGCAACCCGGAACCAACGAGCATTC 1416
Db 1320 GCCACCTGTGGAAGACGACGCGTGTACACAGCAACCCGGAACCAACGAGCATTC 1379
Qy 1417 CACAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTAGGAGCTGTGACCCCTTCGA 1476
Db 1380 CACAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTAGGAGCTGTGACCCCTTCGA 1439
Qy 1477 TCCTGAGCGGTAGTTTTCAACCTCCCTTGCCTTCTGCTTCTGCTCAGGCTGCTC 1536
Db 1440 TCCTGAGCGGTAGTTTTCAACCTCCCTTGCCTTCTGCTTCTGCTCAGGCTGCTC 1499
Qy 1537 CTCCTTAGGACTTTGGGTCAGTTTTGCTTCTGCTTCTGATGTGATAGCGCTCAC 1596
Db 1500 CTCCTTAGGACTTTGGGTCAGTTTTGCTTCTGCTTCTGATGTGATAGCGCTCAC 1559
Qy 1597 CTCACAGCGCTTCTCTGTTTCCAGGACCAACAGAGCTAAGGAATCAGTCAATTCCT 1656
Db 1560 CTCACAGCGCTTCTCTGTTTCCAGGACCAACAGAGCTAAGGAATCAGTCAATTCCT 1619
Qy 1657 GTTGCTTTCTCCAGGAAGCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATGTTTCCTT 1716
Db 1620 GTTGCTTTCTCCAGGAAGCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATGTTTCCTT 1679
Qy 1717 TGTGTGGAAGGTGCTGCTCCAGCTCCAGCTCCCTCTGATGGAAGATAAAACTGCT 1776
Db 1680 TGTGTGGAAGGTGCTGCTCCAGCTCCAGCTCCCTCTGATGGAAGATAAAACTGCT 1739
Qy 1777 GGTGCTTGTGACTGCTGCTGAGCAATCTGAACTTTGGGATGAAGAGCTAAAGTCTT 1836
Db 1740 GGTGCTTGTGACTGCTGCTGAGCAATCTGAACTTTGGGATGAAGAGCTAAAGTCTT 1799
Qy 1837 TGGGCTTTGTTTAACCTTATTTACTGTGCTCCCAAAATCCCTTAGTCCCTTGGGTCAATTT 1896
Db 1800 TGGGCTTTGTTTAACCTTATTTACTGTGCTCCCAAAATCCCTTAGTCCCTTGGGTCAATTT 1859
Qy 1897 AAACATTTTGACTTAAAA 1915
Db 1860 AAACATTTTGACTTAAAA 1878

RESULT 9
ADZ00206
ID ADZ00206 standard; cDNA; 1878 BP.
XX
AC ADZ00206;

XX 30-JUN-2005 (first entry)
XX Mouse Ret ligand 3 (RetL3) partial cDNA, SEQ ID NO:14.
XX Cell growth; development; signal transduction; neurological disease;
XX renal disease; genitourinary disease; neuroprotective; nephrotropic;
XX cancer; neoplasm; cytotatic; RetL3;
XX Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
XX GDNF family receptor alpha 3; GFRA3; ss.
XX Mus sp.
OS
XX Key Location/Qualifiers
XX CDS 205..1245
FT /*tag= a
FT /partial
FT /product= "Mouse RetL3 fragment"
FT /note= "No start codon given"
XX US2005080235-A1.
XX 14-APR-2005.
XX 23-SEP-2003; 2003US-0068936.
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.
XX 23-AUG-1996; 96US-0023444P.
XX 11-APR-1997; 97US-0043533P.
XX 07-MAY-1997; 97WO-US007726.
XX 06-NOV-1998; 98US-00187906.
XX (SANI/) SANICOLA-NADEL M.
XX (HESS/) HESSION C.
XX (CATE/) CATE R L.
XX (WORL/) WORLEY D S.
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX WPI; 2005-305025/31.
XX P-PSDB; ADZ00207.
XX New polypeptide sequence that interacts with a receptor protein Ret to
XX trigger dimerization or autophosphorylation, useful in preparing a
XX composition for treating neurodegenerative disorders, e.g., Alzheimer's
XX disease.
XX Disclosure; SEQ ID NO 14; 67pp; English.
XX The invention relates to the murine and human RetL3 (Ret ligand 3)
XX proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
XX 80% identical to murine or human RetL3. The invention also discloses
XX other RetL proteins such as rat RetL1, human RetL1, human RetL2,
XX fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
XX encoding these RetL proteins or protein fragments. Like other RetL
XX proteins, the RetL3 proteins of the invention interact with the Ret
XX receptor tyrosine kinase that is encoded by the Ret proto-oncogene.
XX triggering Ret receptor dimerization or autophosphorylation. The Ret
XX receptor is expressed during development in a variety of tissues,
XX including the peripheral and central nervous systems and the kidney. It
XX is also expressed in some cancers. RetL proteins such as the murine and
XX human RetL3 proteins, and RetL polynucleotides may be used for
XX stimulating Ret receptor signaling, thereby promoting renal or neuronal
XX cell growth or survival and minimizing damage to such tissues after
XX various insults. They may therefore be used to treat renal disorders
XX (e.g., renal failure, renal tube defects and renal trauma) or
XX neurological disorders including neurodegenerative disorders (e.g.,
XX Alzheimer's disease), bacterial or viral diseases of the nervous system
XX (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
XX or trauma) and developmental neural disorders (e.g., mental retardation).
XX Conversely, antibodies against RetL may be used to block RetL-Ret

XX AAV99331;
AC
XX
XX 25-MAR-1999 (first entry)
DE
XX cDNA encoding a GDNFR-alpha-related protein 3 (GRR3).
XX
XX Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;
KW Glial cell line-derived neurotrophic factor; GDNF; neurotrophin;
KW signal transduction; dopaminergic nerve cell; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurological disorder; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
KW gene therapy; GDNFR-related protein 3; GRR3; ss.
XX
XX Rattus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 67..1260
FT FT /*tag= a
FT FT /product= "GRR3"
XX
XX WO9854213-A2.
XX
XX 03-DEC-1998.
XX
XX 27-APR-1998; 98WO-US008486.
XX
XX 30-MAY-1997; 97US-00866354.
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D;
PI
XX
XX WPI; 1999-080806/07.
DR P-PSDB; AAW84182.
XX
XX New isolated glial cell line-derived neurotrophic factor receptors - used
PT to develop products for treating e.g. improperly functioning dopaminergic
PT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
PT lateral sclerosis.
XX
XX Disclosure; Fig 17; 318pp; English.
XX
XX The present sequence encodes a rat glial cell-line derived neurotrophic
CC factor receptor (GDNFR)-related protein 3 (GRR3). The protein has similar
CC functions to GDNFR. GDNFR proteins are functionally characterised by the
CC ability to bind glial cell line-derived neurotrophic factor (GDNF) and/or
CC neurotrophin specifically, and to act as part of a molecular complex which
CC mediates or enhances the signal transduction affects of GDNF and/or
CC neurotrophin. The proteins can be used for treating improperly functioning
CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
CC amyotrophic lateral sclerosis. They can also be used for treating
CC neurological disorders associated with diabetes, glaucoma or other
CC diseases and conditions involving retinal ganglion cell degeneration,
CC sensory neuropathy caused by injury to, insults to, or degeneration of,
CC sensory neurons, pathological conditions, or disease or injury-related
CC retinopathies. The products can also be used for detection, diagnosis,
CC drug screening and gene therapy
XX
SQ Sequence 1699 BP; 341 A; 556 C; 443 G; 359 T; 0 U; 0 Other;

Query Match 67.4%; Score 1304.4; DB 2; Length 1699;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 161; Indels 44; Gaps 7;
7;
QY 28 GGCACGAGCGCGCGCCAGCGCAGGAGCGTGTGCGATCCGGGCGTCC--ACCC 85
DB 4 GCGCGGTGACACGACGCCGACGACGAGCGGTGCGGGTCCGGCGGTCCAGACCC 63
QY 86 GCCATGGGGCTCTCTCGGAGCCCGGACCTCCACTGCTGANGATCTGCTACTGTGCTG 145
DB 64 GCCATGGGGCTCTCTCGGAGCCCGGACCGCGCGGTAGTGTCTGCTACTGTGCTG 123

QY 146 TCGTTGTGGCTGCCACTTTGGAGCAGGAAACTCCCTTGGCCACAGAGAACAGGTTGTGAAC 205
DB 124 TCGCTGTGGCTACCCCTTTGGAACAGGAAACTCCCTTCCACAGAGAACAGGCTTTGTGAAC 183
QY 206 AGCTGTATCCAGGCGCAGAAAGAAATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACACAG 265
DB 194 AGCTGTATCCAGGCGCAGAAAGAAATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACACAG 243
QY 266 CACCTGGGCTCTCTGCACTTCAGTTTAAAGCAGGGCGTGCCTTTAGAGGAGTCTGCCATG 325
DB 244 CACCTGGAGCTCTCTGCACTTCAGCAGTCCACTGCTGCGCTTCAGGGAGTCTGCCACA 303
QY 326 TCTGCAGACTCCCTAGAGGCGCAGAACAACTCAGGAACAGCTCTCTATAGACTGACAGG 385
DB 304 TCTGCAGGCTGCTTGAAGCAGCAGCACTCAGGAACAGCTCTCTATAGACTGACAGG 363
QY 386 TGCCATCGGCGCATGAAGCACCAAGCTACCTGTCTGGACATTTATTTGACCGTTCAACCT 445
DB 364 TGCCACCGGCGCATGAAGCACCAAGCTACCTGTCTGGACATTTATTTGACCGTTCAACCT 423
QY 446 GCGCGAGGCTTGGTGACTACAGTTGGATGTCTCACTTATGAAGACACAGTGAACG 505
DB 424 GTCCGAAGCCTTGGTGACTACAGTTGGATGTCTCACTTATGAAGACACAGTGAACG 483
QY 506 AAACCTTGAAAAATGAATCTTAGCAAGTTTGAACATGCTCAAAACAGACTCCGAGCTCTGC 565
DB 484 AAACCTTGAAAAATGAATCTTAGCAAGTTTGAACATGCTCAAAACAGACTCCGAGCTCTGC 543
QY 566 CTCAAATTTGCTATGCTGTGTACTCTTCAAGCAAGTGTGACCGCTTCGCAAGGCTTAC 625
DB 544 CTCAAATTTGCTATGCTGTGTACTCTTAAACGACAGTGCAGCCGCTCCGAAAGGCTTAC 603
QY 626 GGGGAGGCGATCTCAGGGATCCGCTGCAGCGCCACCTCTGCTAGCCAGCCAGCTGGCTCC 685
DB 604 GGGGAGGCGTGTCTCAGGGATCCGCTGCAGCGCCACCTCTGCTAGCTCAGCTGGCTCC 663
QY 686 TTCTTTGAGAGGCGCAGAGTCCAGCTCAGAGTGTGCTGTGCTGTGCTGTGCTGTGACCA 745
DB 664 TTCTTTGAGAGGCGGCGAGTCCACCTCAGGGCTGTGCTGTGCTGTGCTGTGCTGTGACCC 723
QY 746 GAAGATCGGGCTGTGGGGAGCGGCGGTAAACACCATTCGCCCCCGCTTGGCGCTGTGCT 805
DB 724 GAAGATCGGGCTGTGGGGAGCGGCGGTAAACACCATTCGCCCCCGCTTGGCGCTGTGCT 783
QY 806 TCTGTAAACCCCAATTTGCTGTGATCTGCGGAGCTTCTGCTGTGCGGAGCTTTGTGCGA 865
DB 784 TCTGTGGCGCCCAACTGCTTAGATCTTGGAGCTTCTGCGGTGCGGAGCTTGTGCGA 843
QY 866 TCAGCGCTGTAGTGGACTTCCAGACCCACTGTCTATGAGACATCTTGGGACTTGTGCA 925
DB 844 TCAGCGCTGTAGTGGACTTCCAGACCCACTGTGCACTTATGAGACATCTTGGGACTTGTGCA 903
QY 926 ACTGAGCAGTCCAGATGTCTCGGGCAATCTGCGGGCTGTATTTGGGACTTGCATGACCCCA 985
DB 904 ACTGAGCAGTCCAGATGTCTCGGGCAATCTGCGGGCTTAAATTTGGGACTTGCATGACCCCA 963
QY 986 AACTTTCATCAGCAGGTCAACACTACTTGTGCTTTAGCTGCACTGCGGAGGCGGCG 1045
DB 964 AACTTTCATCAGCAGGTCAACACTACTTGTGCTTTAGGCTGTACTGCTCGGAGGCGAGTGGC 1023
QY 1046 AACTTTCATCAGGACGAGTGTGAACAGCTGGAAGAGTCTTCTCCAGAACCCCTGCTCGCTG 1105
DB 1024 AACTTTCATCAGGACGAGTGTGAACAGCTGGAAGAGTCTTCTCCAGAACCCCTGCTCATG 1083
QY 1106 GAGGCAATTCAGCTTAAGATCGTTTTCCACAGACAGCTTTCTCCAGAGCTGGGCGAGAC 1165
DB 1084 GAGGCAATTCAGCTTAAGATCGTTTTCCACAGACAACTCTTCTCCAGAGCTGGGCGGAC 1143
QY 1166 TCTACTTTTTCAGTGTGTGACGACGACGACAACTCTGCTCTGAGACTGACGCCAGG 1225
DB 1144 TCTACTTTTTCAGTGTGTGACGACGACGACAACTCTGCTCTGAGGCCCGCAGCTCAGG 1203

QY 1226 CTACCAATCTTTCTTTCTCCATCTCCCTTGTATCTGTGACAGACCTCTGTGTAGCTG 1285
Db 1204 CTACCGGTCTGTCTTTCTTCTATCTCTTGTATCTGTGACAGACCTCTGTGTAACTG 1263
QY 1286 GGCCTTCTCAGGCTCTTTGCTCTCTCCACACACCCAGACTGATTTGCAGCCTGTGTG 1345
Db 1264 GGCCTCCTCAGGCTCTTTGCTCTCTCCACACACCCAGACTGATTTGCAGCCTGTGTG 1323
QY 1346 GGAGAGAACTCCGCCAGCTGTGGAAAGAGACGACGCTGTCTACACAGCAACCCGGAACCA 1405
Db 1324 GGAGAGAAATGCTGGCTCTGGAGAGAGATGCAACAGGCTCA----- 1367
QY 1406 ACCAGCATTCGCGAGCAGATCCCTGCTGTCTCCAGAGAGTCTTT---AGAGTGAAGGC 1462
Db 1368 -----CTGCAATCTCTGCTCTCCAGATGAGTCTTTGGAGAAGCGAGGCG 1414
QY 1463 TGTGACCTTCGG-ATCCGTGAGCGGCTAGTTTTCAACTCCCTGCGCCCTGCTTCCTTC 1521
Db 1415 TGTGACCGTTCAGAAATCTTGAGCGGCGAGCTTTCAAACTCTCTCTAC-----TTACTC 1467
QY 1522 TGGCTCAGGCTCTCTCTTAGGACTTTTGTGGTCCAGTTTGTCTTCTGTCTGTATGG 1581
Db 1468 CTGCTTGGCTCTCTCTCCAGGACCTGT-ACTCCAGTTTGGCTGTATATTTGGTGG 1526
QY 1582 TGATTAGGCGCTCACTCCAGGCTTCTTCTGTTTCCAGACCAACAGGCTTAAGG 1641
Db 1527 TGATTAGCTTCCAGCTCCAGGCTTCTTCTGTTTCCAGACCAACAGGCTTAAGG 1585
QY 1642 ATGAGTCAATCCCTGTTGCTTCCAGGAGGAGGCTAAGGTTCTGAGGTGACCTGA 1701
Db 1586 ACTCACTCATTCCTGTTGCTTCTCCAGGAAGGAGGCTGAGGTTCTGAGGCGAGCTGA 1645
QY 1702 GAAAAATGTTCTTTGTTGGAAGCGTGTCTCCAGCC 1741
Db 1646 GAAAGATGTTCTTTGTTGAGGAAGGCTGTGTGTTCCAAACC 1685

RESULT 11
ID AAV99334 standard; cDNA; 1878 BP.
XX AAV99334;
XX AC AAV99334;
XX DT 25-MAR-1999 (first entry)
XX DE Glial cell line-derived neurotrophic factor receptor gamma 2 cDNA.
XX KW Glial cell line-derived neurotrophic factor receptor gamma 2;
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte; db.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 68..1270
FT /*tag= a
FT /product= "GDNFR-gamma2"
FT sig_peptide 68..160
FT /*tag= b
FT mat_peptide 161..1267
FT /*tag= c
XX FT
XX PN WO9853069-A2.
XX PD 26-NOV-1998.
XX PF 20-MAY-1998; 98WO-US010328.
XX PR 20-MAY-1997; 97US-0047092P.

PR 27-JUN-1997; 97US-00884638.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Ni J, Hsu T, Young P, Gentz RL, Ruben SM;
XX WPI; 1999-070150/06.
XX P-PSDB; AAW84186.
XX New isolated glial cell derived neurotrophic factor receptors - used to
XX develop products for treating e.g. neurodegenerative disorders,
XX schizophrenia, hypertension, tumours, renal disorders, kidney failure or
XX gut dysfunction.
XX Claim 52; Fig 7A-D; 156pp; English.
XX The present sequence encodes a glial cell line-derived neurotrophic
XX factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
XX with GDNFR-alpha, which is capable of complexing with glial cell line-
XX derived neurotrophic factor (GDNF) and mediating cell response to GDNF.
XX The GDNFR polypeptides and agonists can be used for treating disorders
XX associated with decreased activity of the respective polypeptides. They
XX can be used for treating neurodegenerative diseases such as amyotrophic
XX lateral sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive
XX dyskinesia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid
XX tumour, renal disorders, kidney failure, gut dysfunction, or for
XX regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of
XX the polypeptides can be used for treating disorders associated with
XX increased activity of the respective polypeptides. The products can also
XX be used for detection, diagnosis and drug screening
XX Sequence 1878 BP; 391 A; 617 C; 477 G; 393 T; 0 U; 0 Other;
XX
XX Query Match 49.4%; Score 955.2; DB 2; Length 1878;
XX Best Local Similarity 73.5%; Pred. No. 8.8e-245;
XX Matches 1380; Conservative 0; Mismatches 408; Indels 90; Gaps 9;
QY 83 CCCGCCATGGGGCTCTCTGTGAGCCCGGACCTC-----CACTGCTGATGATCTGTG 133
Db 62 CTCGCCATGGTGGCGCCCTGAAACCGCGACCGCTGCCGCCGCTAGTCTGATGTGTCTG 121
QY 134 CTACTGTGTCTGTGTGTGTGCTGCCACTTGGAGCGGAAACTCCCTTGCACAGAGAAC 193
Db 122 CTGCTGTGCGCGCGCTGCTCTGCTGCGGAGACCCCTTCCACAGAAAGC 181
QY 194 AGTTTGTGAACAGCTGTACCCAGCGCAAGAAATGCCAGGCTAATCCCGCTTGCAAG 253
Db 182 CGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAGTGCCAGGCTGATCCCACTGCAGT 241
QY 254 GCTGCTTACAGCACCTGGGGCTCTGCACTTCCAGTTTAAAGCAGGCGCTGCGCTTAGAG 313
Db 242 GCTGCTTACCAACCACTGGATTCTGCACTTCTAGCATAGCACCACCACTGCCCTCAGAG 301
QY 314 GAGTCTGCCATGTCTGCAGACTGCTAGAGCGCAGACCAACTCAGAAACAGCTCTCTG 373
Db 302 GAGCTTTCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
QY 374 ATAGACTGCAGTGCCATCGGCGCATGAAGCAACCAAGCTACTCTGTCTGGAATTTATTGG 433
Db 362 ATAGCTGTGATGTGCCACCGCGCATGAAGAACAGGTTGCTGCTGTTGGACATCTATTGG 421
QY 434 ACCGTTCACTGCTGCCGAGCGCTTGGTGACTTACGAGTTGGATGTCTACCTTATGAAGAC 493
Db 422 ACCGTTCACTGCTGCCGAGCGCTTGGTAACTATGAGCTGGATGTCTCTCCCTTATGAAGAC 481
QY 494 ACAGTGACCAACCACTGGAATTAATCTTACAGTTGAACTGCTCAAAACAGAC 553
Db 482 ACAGTGACCAACCACTGGAATTAATCTTACAGAACTGAACTGCTCAAAACAGAC 541
QY 554 TCGGACCTCTGCTCAAAATTTGCTATGCTGTGTAATCTTTCACGAAAGTGTGACCGCTG 613
Db 542 TCAGACCTCTGCTCAAGTTTGGCAATGCTGTGTACTCTCTCAATGACAACTGTGACCGGCTG 601

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QY 614 CGCAAGGCTACGGGAGGCAATGCTCAGGATCCGCTCCAGCGCCACTCTGCTAGCC 673
Db 602 CGCAAGGCTACGGGAGGCGGTCTCCGGGCCCACTGCGAGGCCAAGTCTGCTCAGG 661
QY 674 CAGTGCCTCTCTTTTGAAGGAGCAGAGTCCCAAGCTCAGGCTCTGCTGCTGT 733
Db 662 CAGTGCCTCACTTTCTTGAGAAGGCCGCGAGCCCAACGCGCAGGGCTGCTACTGTGC 721
QY 734 CCCTGTGCACAGAAGATGCGGCTGTGGGAGCGGCGGTAAACACCATGCCCCAGT 793
Db 722 CCATGTGCCCCCAACGACCGGGCTGTGGGAGCGCGCGCAACACCATGCCCCAAC 781
QY 794 TCGCGCTGCTCTCTGTAACCCCAATGCTGAGATCTGCGAGCTTCTGCGGTGCGAG 853
Db 782 TCGCGCTGCTGCGCTCTGCGCCCCCAACTGCTGTGAGCTGTGGGCGCTCTGCTTCCGAC 841
QY 854 CTTTGTGTGAGATCAAGCTGATGAGCTTTCAGACCCCACTGTCATCTATGAGACATCCTT 913
Db 842 CCGCTTTGAGATCAGCGCTGCTGGATTTTCAGACCCCACTGTCATCTGAGACATCCTA 901
QY 914 GGGACTGTGCAACTGAGAGTCCAGATGTCTGCGGCAATACCTGGGCTGATGGACT 973
Db 902 GGAATCTGTGCAACAGAGAGTCCAGATGTCTACGAGCATACCTGGGCTGATGGGACT 961
QY 974 GCATGACCCCAAACTTCATCAGCAAGGTCAACACTACTGTTGCTTAAAGCTGCACCTGC 1033
Db 962 GCATGACCCCAAACTTTGTAGCAATGTCAACAGTGTTCCTTAAAGCTGCACCTGC 1021
QY 1034 CGAGGACGGCAACTCAGGACGAGTGTGAACAGCTGGAAGTCTCTTCCAGAAC 1093
Db 1022 CGAGGACGGCAACTCAGGACGAGTGTGAATGCTGGAAGTCTCTTCCCAAC 1081
QY 1094 CCTGCTGCTGGAGGCCAATTCAGCTAAGATGCTTTCCAGACAGCTCTTCTCCAG 1153
Db 1082 CCTGCTGCTGAGGAGCCATTGCACTAAGATGCGTTTTTCAGCCAACTCTTCTCCAG 1141
QY 1154 GACTGGGAGACTCTACTTTTTTCACTGGTGAGCAGCAGAACAGCAACCTGCTCTGAGA 1213
Db 1142 GACTGGCACAACCTTCTGCTGTGATGGCAGACCAAGATGAACCTGCTGTGAGG 1201
QY 1214 CTCGAGCCAGGCTACCCATCTTTCTTCTCCATCTCTTCCCTGATCTGCTGAGACC 1273
Db 1202 CCACAGCCCTGGGTGCTCTCTTTCTCTGACGCTTCCCTGATCTGCTCTGAGC 1261
QY 1274 CTCCTGTAGCTGGCTTCTCAGGCTCTTGTCTCTCTCCACACACCCAGACTGATTTG 1333
Db 1262 CTATGCTAGCTGAGCTTCCCAAGGCCCTCT-TCCCTCTCCACACACCCAGGCTGACTTG 1320
QY 1334 CAGCTGTGGTGAGAGAACTCGCGAGCTGTGGAAGAGCAGCGTGTACACAGC 1393
Db 1321 CAGCCACACAGGGGTGAGGAAGGACAGCAGCAGGAGAGGTGAGTGGCAGATGAGG 1380
QY 1394 AACCGGAACCAACGAGCAATTCGCGAGCACAATCCGCTGTCTCCAGAGAGGCTCTAGA 1453
Db 1381 GCACAGG-----AGGAGG-----AGA 1390
QY 1454 AGTGAGGCTGTGACCTTCCGATCTGTAGGCGCTAGTTTTCAACCTCCCTTGGCCCTG 1513
Db 1391 AGCTAAGGGTATGACCTCCAGATCTTACTGCTCCAGCTCTCAATTCCTCCACCCCATC 1450
QY 1514 CTTCTCTGCTGAGCTGAGCTCTCTTAGGACTTTGTGGGTCCAGTTTGGCTTCTGT 1573
Db 1451 TCACCTTCTGATCTGCTGCCCCCTC-----CTTGTGGCCACAAATTTAGCAATGCA 1503
QY 1574 TCTGATGTGATTTAGGGCTCACTCTC-----AGCGCTTCTTCTGTTTCCAGGAC 1625
Db 1504 TCTGTGTGTGACAGCTCCACCAAGCCCCCTTCTGAGGCCCTTCTCTGACTACCAAGAT 1563
QY 1626 CACCACAGGCTAAGGATCAGTCACTCCCTGCTTGGCTTC-----TCCAGGAG 1674
Db 1564 CA-CCAGATCTAATAAGTTAGCCATTTCTTATTCATTTCCAGATTAAGGTTAGGTTAGG 1622
QY 1675 GCAGCTAAGGGTCTCTGAGTGAAGTGAAGAAATGTT-TCCCTTGTGTGGAAGGCTGTGTG 1733
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Db 1623 GAGGACTGGGTGTTCTGAGGCGAGCTAGAAAGTCAATTCCTCTTGTGAAGAGGCTCTG 1682
QY 1734 CTCAGGCTCCAGCTCCCTCTGAATGAAGATAAAACCTGCTGCTGCTGACTGCTCT 1793
Db 1683 CCCCCTGCTCTCC--TCTCTGAGTGGAGGATGAAAACCTACTGCTGCACTGCCCTGTC 1740
QY 1794 GCCAGGCAATCTCAACATTTGGGCGATGAAGAGCTAAAGTCTTTGGGTCTTTGTTAACTC 1853
Db 1741 CCGGATCTCTCCGAACATCTGGGCATCAGGAGCTGGAGCTGTGGGCTTGTCTTTATTC 1800
QY 1854 CTATTACTGTCCCAAAATTCCTTAGTCCCTTGGGCTCATGATTAACAATTTTGACTTAAA 1913
Db 1801 CTATTATGTCTAAAGTCTCTCTGGGCTCTTGGGCTCATGATTAACCTTTGACTTAAA 1860
QY 1914 AAAAAAAAAAAAAAAAAA 1931
Db 1861 AAAAAAAAAAAAAAAAAA 1878

RESULT 12
AAZ93702
ID AAZ93702 standard; cDNA; 1829 BP.
AC AAZ93702;
XX
XX 16-AUG-2000 (first entry)
XX
XX PRO538 DNA48613-1268.
DE
XX Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
KW leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 38..1240
XX /*tag= a
XX /product= "PRO538 polypeptide"
XX
XX WO200021996-A2.
XX
XX 20-APR-2000.
XX
XX 05-OCT-1999; 99WO-US023089.
XX
XX 13-OCT-1998; 98US-0104080P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
XX Yuan J;
XX
XX WPI; 2000-317943/27.
XX
XX P-PSDB; AAY83226.
XX
XX Composition for inhibiting neoplastic cell growth and treating cancers of
XX ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
XX PRO538, PRO172 or PRO182 polypeptide or their agonist.
XX
XX Disclosure; Fig 5; 122pp; English.
XX
XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
XX polypeptide or their agonists, mixed with a carrier is useful for
XX inhibiting neoplastic growth and treating tumors such as cancers of
XX breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
XX central nervous system, melanoma and leukaemia
XX
XX Sequence 1829 BP; 364 A; 607 C; 467 G; 391 T; 0 U; 0 Other;
XX
XX Query Match 48.3%; Score 934.6; DB 3; Length 1829;
XX Best Local Similarity 73.3%; Pred. No. 2.9e-239;
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Matches 1357; Conservative 0; Mismatches 404; Indels 90; Gaps 9;

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QY 83 CCGCCATGGGGCTCTCTCTGAGACCGCGACCTC-----CACTGCTGATGATCTCTG 133
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 32 CTGCGCATGGTGGCGCCCTGAAACCGCGACCGCTGCCCGCGTAGTCTCTGATGTTGCTG 91
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 CTACTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 193
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 92 CTGTGTCTGCGCGCTGCGCGCTGCTCTCTGAGCGGAGACCCCTTCCACAGAAAGC 151
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 AGGTTGTGAACAGCTGTACAGGCCAGAAAGAAATGCGAGCTAAATCCCGCTTGCAAG 253
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 CGACTCATGAACAGCTGTCTTCAGGCCAGAGAAAGTCCAGCTGATCCCACTGTCAGT 211
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 254 GCTGCTTACAGCACCTGGGCTCTCTGACCTCAGTTTAAAGCAGGCGCTGCGCTTAGAG 313
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 GCTGCTTACCAACACTGATTTCTGCACTCTAGCATTAAGCAACCCCACTGCGCTCAGAG 271
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 314 GAGTGTGCATGTCTGCACTGTCTTAGAGGAGCGAGAAACAACTCAGAGAAAGCTCTGTG 373
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 GAGCTTCTGGTCCCTGCTGACTGCTGAGGAGCAGACAACTCAGGAAACAGCTCTCTG 331
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 374 ATAGACTGAGTGGCATCGGCGCATGAAGCCCAAGCTACCTGTCTGAGACATTTATTGG 433
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 ATAGGCTGATGTGCCACCGCGCATGAAGAACCAAGTTGCGTGTGGACATCTATTGG 391
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 434 ACGTTTACCTGCCCGAAGCCTTGGTGACTAGAGTTGGATGTCTCACCTATCAAGAC 493
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 392 ACGTTTACCTGCCCGAAGCCTTGGTAATCTATAGCTGGATGTCTCCCTATAGAGAC 451
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 494 ACAGTGACAGCAAAACCTTGAAGAAATCTTAGCAAGTTGAACATGTCTAAACAGAC 553
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 452 ACAGTGACAGCAAAACCTTGAAGAAATCTCAGCAAACTGAAACATGTCTAAACAGAC 511
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 554 TGGGACTTGTCTGCTGAATTTGCTATGCTGTGATCTCTTCAAGCAAGTGTACCGCTG 613
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 512 TCAGACCTTGTGCTCAAGTTTGTGCTGCTGTGATCTCTCAATGACAAAGTGTACCGCTG 571
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 614 CGCAGGCTTACGGGAGGAGCATGTCTCAGGGATCCGCTGCCAGCGCACCTCTGCTTAGCC 673
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 572 CGCAGGCTTACGGGAGGAGGCTGTCTCCGGGCCCATCTGCCAGGCGCACCTCTGCTCAGG 631
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 674 CAGCTGCGTCTCTTTTGAAGAGGAGCAGAGTCCACGCTCAGGGTCTGTGCTGTGT 733
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 632 CAGCTGCTCACTTTCTTCAGAAAGGCGCGAGCCACCGCAGGCGCTGTACTGTGC 691
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 734 CCTGTGCAACCAAGATCGGGCTGTGGGAGCGGCGGCTAAACCATCGCCCCCAGT 793
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 692 CCATGTGCCCCCAACGACCGGGGCTGCGGGGAGCGCGGCGCAACACCATCGCCCCAAC 751
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 794 TGGCGCTGCTCTCTGTAACCCCAATTCCTTGGATCTCGGAGCTTCTGCGGTGGGAC 853
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 752 TGGCGCTGCGGCTGTGGCCCTCCAACTGCTGTGAGCTGCGGGCTCTGCTCTCCGAC 811
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 854 CCTTTGTGAGATCAGCGCTGATGGAATTCAGACCCACTGTCTATGAGACATCTCTT 913
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 812 CCGCTTTGAGATCAGCGCTGTGGATTTCCAGACCCACTGTGCCATCCCATGACATCTTA 871
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 914 GGGACTTGTGCAACTGAGCAGTCCAGATGTCTCGGGGATACCTGGGGCTGATGGGACT 973
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 872 GGAACTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCTGGGGCTGATGGGACT 931
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QY 974 GCATGACCCCAAACTTCAATCAGCAGAGTCAACACTACTGTGTGCTTAACTGACCTGC 1033
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 932 GCATGACCCCAAACTTGTGAGCAATGTCAACACAGTGTGGCTTAACTGACCTGC 991
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1034 CGAGCAGCGGCAACCTACAGGACGAGTGTGAACAGCTGGAAGGCTCTTCTCCAGAAC 1093
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 992 CGAGGCAGTGGCAACCTCGAGGAGGAGTGTGAATGTCTGGAAGGTTCTTCTCCACAC 1051
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1094 CCTGTGCTGTGAGGACCAATTGAGCTAAGTGGCTTCCACAGACAGCTCTTCTCCGAG 1153
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QY 1052 CCTGTGCTTACGAGGACCAATTGAGCTAAGTGGCTTTCACAGGCAACTCTTCTCCGAG 1111
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RESULT 13

AAA88519

ID AAA88519 standard; cDNA; 1829 BP.

XX

AC AAA88519;

XX 22-JAN-2001 (first entry)

XX

XX Human PRO538 cDNA clone DNA48613-1268.

XX

XX

XX

XX

KW PRO538; human; ocular disease; retinopathy; maculopathy; therapy;

KW retinitis pigmentosa; macular degeneration; retinal detachment;

KW retinal tear; macular hole; myopia; traumatic choriorretinopathy;

KW acute retinal necrosis syndrome; contusion; edema;

KW retinal vision occlusion; vascular disease; retinal vasculitis;

KW thrombocytopenic purpura; uveitis; retinal occlusion; GFR-alpha-3; ss.

XX Homo sapiens.

XX

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1935	100.0	1935	9	US-10-621-855-4	Sequence 4, Appli
2	1887	97.5	1889	9	US-10-668-936-16	Sequence 16, Appl
3	1867	96.5	1878	9	US-10-668-936-14	Sequence 14, Appl
4	1304.4	67.4	1899	8	US-10-872-161-41	Sequence 41, Appl
5	934.6	48.3	1829	3	US-09-828-368-15	Sequence 15, Appl
6	934.4	48.3	1792	9	US-10-621-855-14	Sequence 14, Appl
7	933	48.2	1991	8	US-10-872-161-37	Sequence 37, Appl
8	897.6	46.4	1699	9	US-10-668-936-20	Sequence 20, Appl
9	854.4	44.2	1203	3	US-09-220-920-65	Sequence 65, Appl
10	852.8	44.1	1203	8	US-10-482-029-274	Sequence 274, Appl
11	751.6	38.8	1271	9	US-10-668-936-18	Sequence 18, Appl
12	749.8	38.7	1837	9	US-10-621-855-16	Sequence 16, Appl
13	385.4	19.9	387	9	US-10-621-855-1	Sequence 1, Appli
14	331	17.1	353	9	US-10-621-855-2	Sequence 2, Appli
15	218.4	11.3	260	6	US-10-305-720-530	Sequence 530, App
16	169.8	8.8	238	6	US-10-305-720-537	Sequence 537, App
17	102	5.3	1392	3	US-09-388-316-2	Sequence 2, Appli
18	102	5.3	1392	5	US-10-357-822-2	Sequence 2, Appli
19	102	5.3	1490	7	US-10-673-007-10	Sequence 10, Appl
20	102	5.3	1888	9	US-10-668-936-12	Sequence 12, Appl
21	102	5.3	1995	3	US-09-388-316-15	Sequence 15, Appl
22	102	5.3	1395	5	US-10-357-822-15	Sequence 15, Appl
23	102	5.3	2600	3	US-09-388-316-1	Sequence 1, Appli

QY 1729 TGGTGTCTCAGGCTCCAGCTCCCTCTGAATGGAAGATAAAAAACCTGCTGCTGTCTTGACT 1788
Db 1681 TGGTGTCTCAGGCTCCAGCTCCCTCTGAATGGAAGATAAAAAACCTGCTGCTGTCTTGACT 1740
QY 1789 GCTCTGCCAGGCAATCCTGAACATTTGGGCATGAAGCTAAAGTCTTTGGGTCTTGTTT 1848
Db 1741 GCTCTGCCAGGCAATCCTGAACATTTGGGCATGAAGCTAAAGTCTTTGGGTCTTGTTT 1800
QY 1849 RACTCTATTACTGTCCTCAAAATCCCTAGTCCCTTGGGTCAATGAATTAACATTTTGAC 1908
Db 1801 AACTCTATTACTGTCCTCAAAATCCCTAGTCCCTTGGGTCAATGAATTAACATTTTGAC 1860
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAA 1935
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 3

US-10-668-936-14
; Sequence 14, Application US/10668936
; Publication No. US20050080235A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS: 21
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..1242
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-668-936-14
Query Match 96.5%; Score 1867; DB 9; Length 1878;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 37 CGCGCGCGCCAGCCAGGCGCTGTGCATCCCGGGCGTCCACCCGCCATGGGGCT 96
Db 1 CGCGCGCGCCAGCCAGGCGCTGTGCATCCCGGGCGTCCACCCGCCATGGGGCT 60
QY 97 CTCTGGAGCCCGGAGACCTCCACTGTGTGATGATCTGTCTACTGTGTGTGTGTGTGCT 156
Db 61 CTCTGGAGCCCGGAGACCTCCACTGTGTGATGATCTGTCTACTGTGTGTGTGTGTGCT 120
QY 157 GCCACTTGGAGCAGGAACTCCCTTGGCCACAGAGAAAGAGTTTGTGAACAGCTGTACCCTA 216
Db 121 GCCACTTGGAGCAGGAACTCCCTTGGCCACAGAGAAAGAGTTTGTGAACAGCTGTACCCTA 180
QY 217 GCCAGAAAGAAATGCGAGGCTAATCCCGCTTGTCAAGGCTGCCTACCAGCACCTGGGGCTC 276
Db 181 GCCAGAAAGAAATGCGAGGCTAATCCCGCTTGTCAAGGCTGCCTACCAGCACCTGGGGCTC 240
QY 277 CTGCACTCCAGTTTAAGCAGGCGCTGCCCTTAGAGAGAGTCTGCAATGTCTGCAGACTG 336
Db 241 CTGCACTCCAG-TTAAGCAGGCGCTGCCCTTAGAGAGAGTCTGCAATGTCTGCAGACTG 299
QY 337 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAGTGCCTACCGCG 396
Db 300 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAGTGCCTACCGCG 359
QY 397 CATGAAGCACCAGCTACTCTGTCTGGACATTTATTTGGACCGTTTCAACCTGCCGGAAGCT 456
Db 360 CATGAAGCACCAGCTACTCTGTCTGGACATTTATTTGGACCGTTTCAACCTGCCGGAAGCT 419
QY 457 TGGTGACTACAGATTGATGTCTCAACCTATGAAGACACAGTGCAGTGCCTACCAACCTGAA 516
Db 420 TGGTGACTACAGATTGATGTCTCAACCTATGAAGACACAGTGCAGTGCCTACCAACCTGAA 479
QY 517 AATGAATCTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTCCCTCAAAATTCG 576
Db 480 AATGAATCTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTCCCTCAAAATTCG 539
QY 577 TATGCTGTGTACTCTTCAACGACAAAGTGTGACCGCTGCGCAAGGCTTACGGGGAGGCAATG 636
Db 540 TATGCTGTGTACTCTTCAACGACAAAGTGTGACCGCTGCGCAAGGCTTACGGGGAGGCAATG 599
QY 637 CTCAGGGATCCGCTGCGAGCGCACCTCTGCTGAGCCAGCTGCGCTCTTCTTTTGAGAA 696
Db 600 CTCAGGGATCCGCTGCGAGCGCACCTCTGCTGAGCCAGCTGCGCTCTTCTTTTGAGAA 659
QY 697 GGCAGCAGGTCCTCAGCGCTCAGGGTCTGCTGTGTCTGCTGTCCTGTCACCAAGAGATGCGGG 756
Db 660 GGCAGCAGGTCCTCAGCGCTCAGGGTCTGCTGTGTCTGCTGTCCTGTCACCAAGAGATGCGGG 719
QY 757 CTGTGGGAGCGGGCGGTAAACACCATCGCCCCCAGTTTGGCCCTTCTGTAAACCCC 816
Db 720 CTGTGGGAGCGGGCGGTAAACACCATCGCCCCCAGTTTGGCCCTTCTGTAAACCCC 779
QY 817 CAATTGCTGTGATCTGCGAGGCTTCTGCGGTGCGGACCTTTTGTGCAGATCACGCTGAT 876
Db 780 CAATTGCTGTGATCTGCGAGGCTTCTGCGGTGCGGACCTTTTGTGCAGATCACGCTGAT 839
QY 877 GGACTTCCAGACCCACTGTCTCATCTTATGGACATCTCTGGGACTTGTGCAACTGAGCAGTGC 936
Db 840 GGACTTCCAGACCCACTGTCTCATCTTATGGACATCTCTGGGACTTGTGCAACTGAGCAGTGC 899
QY 937 CAGATGTCTGCGGGCATACCTGGGGCTGATTGGGAGTCCCATGACCCCAAACTTCATCAG 996
Db 900 CAGATGTCTGCGGGCATACCTGGGGCTGATTGGGAGTCCCATGACCCCAAACTTCATCAG 959
QY 997 CAGGTCAACACTACTGTGTGCTTAAAGCTGCACTGCGGAGGCGGCAACCTTACAGA 1056
Db 960 CAGGTCAACACTACTGTGTGCTTAAAGCTGCACTGCGGAGGCGGCAACCTTACAGA 1019

1057 CGAGTGTGAACAGCTGGAAAGTCTCTTCCAGAAACCCCTGCTCGTGGAGGCCATTGC 1116
1020 CGAGTGTGAACAGCTGGAAAGTCTCTTCCAGAAACCCCTGCTCGTGGAGGCCATTGC 1079
1117 AGCTAAGATGCGTTTCCAGACAGCTCTTCCAGAGACTGGGAGAGCTCTACTTTTTC 1176
1080 AGCTAAGATGCGTTTCCAGACAGCTCTTCCAGAGACTGGGAGAGCTCTACTTTTTC 1139
1177 AGTGTGACAGCAGCAGCAACAGCAACCCCTGCTCTGAGACTGCAAGCCAGGCTACCCATTCT 1236
1140 AGTGTGACAGCAGCAGCAACAGCAACCCCTGCTCTGAGACTGCAAGCCAGGCTACCCATTCT 1199
1237 TTCTTTTCTCATCTTCCCTTGAATCTGCTGACAGCCCTCTGCTGAGTGGGCTTCCCTCAG 1296
1200 TTCTTTTCTCATCTTCCCTTGAATCTGCTGACAGCCCTCTGCTGAGTGGGCTTCCCTCAG 1259
1297 GGTCTTTGCTCTCTCCACACAGCAGCTGATTTGCAAGCTGCTGAGCTGGGAGAGATC 1356
1260 GGTCTTTGCTCTCTCCACACAGCAGCTGATTTGCAAGCTGCTGAGCTGGGAGAGATC 1319
1357 GCAGCTGTGGAAGAGCAGCGTGTCTACAGCAACCCGGAACCAACAGGCAATC 1416
1320 GCAGCTGTGGAAGAGCAGCGTGTCTACAGCAACCCGGAACCAACAGGCAATC 1379
1417 CGCAGCAGATCCCGTCTGCTCCAGAGAGGCTTTAGAAAGTGAAGGCTGTGACCCCTTCCGA 1476
1380 CGCAGCAGATCCCGTCTGCTCCAGAGAGGCTTTAGAAAGTGAAGGCTGTGACCCCTTCCGA 1439
1477 TCCTGAGGCGTGTGTTTCAACCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1536
1440 TCCTGAGGCGTGTGTTTCAACCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1499
1537 CTCTCTTAGGACTTTGTTGGTCCAGTTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596
1500 CTCTCTTAGGACTTTGTTGGTCCAGTTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
1597 CTCAGCGCTTCTCTCTGTTTCCAGGACCAACCCAGAGGCTAAGAAATCAGTCAATCCCT 1656
1560 CTCAGCGCTTCTCTCTGTTTCCAGGACCAACCCAGAGGCTAAGAAATCAGTCAATCCCT 1619
1657 GTTGTCTTCCAGGACGAGCTAAGGTTCTGAGTGAAGTGAAGAAATGTTTCTT 1716
1620 GTTGTCTTCCAGGACGAGCTAAGGTTCTGAGTGAAGTGAAGAAATGTTTCTT 1679
1717 TGTGTGAAGGCTGTGCTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1776
1680 TGTGTGAAGGCTGTGCTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1739
1777 GGTGTCTTGAAGCTGTGCTCCAGGCAATCCTGAACATTTTGGGCATGAAGGCTTAAAGTCTT 1836
1740 GGTGTCTTGAAGCTGTGCTCCAGGCAATCCTGAACATTTTGGGCATGAAGGCTTAAAGTCTT 1799
1837 TGGGTCTTGTAACTCTCTTACTGTGCTCCAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1896
1800 TGGGTCTTGTAACTCTCTTACTGTGCTCCAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1859
1897 AAACATTTTGAATTTAA 1915
1860 AAACATTTTGAATTTAA 1878

RESULT 4
US-10-872-161-41
; Sequence 41, Application US/10872161
; Publication No. US20040235714A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401D
; CURRENT APPLICATION NUMBER: US/10/872,161

; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/08/866,354
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; PRIOR APPLICATION NUMBER: US 08/837,199
; PRIOR FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1699
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1257)
US-10-872-161-41

Query Match 67.4%; Score 1304.4; DB 8; Length 1699;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 161; Indels 44; Gaps 7;

QY 28 GGCAAGAGCGCGCGCGCCAGCGCAGCAGAGCGCTGTGCGATCCCGGGCGCTCC--ACCC 85
Db 4 GCCCGTTCGACCGCAGCGCCAGCAGCAGCAGAGCGCTGTGCGCGCTCCGCGCGCTCCAGAGCCC 63
QY 86 GCCATGGGGCTCTCTGGAGCCCGCAGCTCCACTGCTGATGATCTCTCTACTTGTGTGTG 145
Db 64 GCCATGGGGCTCTCTGGAGCCCGCAGCGCGCGCTGTGATGATCTCTCTACTTGTGTGTG 123
QY 146 TCGTGTGGCTGCCACTTTGGAGCAGGAAATCTCCCTTGCACAGAGAAACAGGTTTGTGAAC 205
Db 124 TCGTGTGGCTTACCCCTTTGGAAACAGGAAATCTCCCTTCCCAAGAGAAACAGGCTTGTGAAC 183
QY 206 AGCTGTACCCAGGCGCAGAAAGATGCGAGCTAATCCCGCTTGCAGGCTGCTTACCAG 265
Db 184 AGCTGTACCCAGGCGCAGAAAGATGCGAGCTAATCCCGCTTGCAGGCTGCTTACCAG 243
QY 266 CACCTGGGCTCTGCACTCCAGTTTAAAGCAGGCGCTGCGCTTAGAGAGTCTGCCATG 325
Db 244 CACCTGGACTCTGCAACCCCGAGTCTCAGCAGTCCAATGCGCTCAGGGAGTCTGCCACA 303
QY 326 TCTCAGACTGCCCTAGAGGCGCAGAAACATCTCAGGAAACAGCTCTCTGATAGACTGCGAG 385
Db 304 TCTCAGCGTGCCTTGAAGCAGCAGCAACTCAGGAAACAGCTCTCTCATAGACTGCGAG 363
QY 386 TGCATCGGCGCATGAAGCAGCAACAGTACCTGTCTGGAACATTTATGGACCGTTCAACCT 445
Db 364 TGCCACCGCGCATGAAGCAGCAACAGTACCTGTCTGGAACATTTATGGACCGTTCAACCT 423
QY 446 GCCGAGCGCTTGGTGTGACTAGAGTTGATGCTCACCTATGAAGACAGAGTGAACGAGC 505
Db 424 GTCCGAGCGCTTGGTGTGACTAGAGTTGAGCTCTCACCTATGAAGACAGAGTGAACGAGC 483
QY 506 AAACCTTGAAATGAATCTTGAAGTTGAACATGCTCAAAACAGAGTCTCGAGACTCTGTC 565
Db 484 AAACCTTGAAATGAATCTTGAAGTTGAACATGCTCAAAACAGAGTCTCGAGACTCTGTC 543
QY 566 CTCAAAATTTGCTATGCTGTGTACTCTTTCAGCAAGAGTGTGACCGGCTGCGCAGGCTTAC 625
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QY 626 GGGGAGCGATCTCAGGAGTCCGCTGCGAGCGCACCTCTGCTGCTAGCCAGCTGCGCTCC 685
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QY 746 GAAGATGCGGCTGTGGGAGCGGCGGTAAACCATTCGCCCCCGAGTTGGCCCTGTGCT 805

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Db 724 GAAGATCGGGCTGTGGGAGCGCGCGCAACACCATCGCCCCAGTTGGCCCTCCG 783
Qy 806 TCTGTAAACCCCAATGTGCTGTGATCTGCGAGCTTCTGCCGTGGGACCCCTTTGTGCGAGA 865
Db 784 TCTGTGGCCCCCAACTGCTAGATCTTGGAGCTTCTGCCGTGGGACCCCTCTGTGCGAGA 843
Qy 866 TCAGCCCTGTAGGACTTCCAGACCCACTGTCTATATGGACATCTTGGGACTTGTGCA 925
Db 844 TCACGCCCTGTAGTACTTCAGACCCACTGCCACCCCTATGGACATCTCTGGGACTTGTGCA 903
Qy 926 ACTGAGCAGTCCAGATGTCTGGGCGCATACCTGGGGCTGATTGGGACTGCCATGACCCCA 985
Db 904 ACTGAGCAGTCCAGATGTCTGGGCGCATACCTGGGGCTAATTGGGACTGCCATGACCCCA 963
Qy 986 AACTTTCATCAGCAAGGTCAACACTACTGTGTGCTTAAAGCTGACCTGCCGAGGCGAGCGC 1045
Db 964 AACTTTCATCAGCAAGGTCAACACTACTGTGTGCTTAAAGCTGTACTGCGGAGGCGAGTGC 1023
Qy 1046 AACCTTACAGGAGGAGTGAACAGCTGGAAAGTCTTCTCCAGAACCCCTGCTCGTG 1105
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Qy 1106 GAGGCCATTGAGCTTAAGATGGTTTCCACAGACAGCTCTTCTCCAGGACTGGGCGAGAC 1165
Db 1084 GAGGCCATTGAGCTTAAGATGGTTTCCACAGACAGCTCTTCTCCAGGACTGGGCGAGAC 1143
Qy 1166 TCTACTTTTTCAGTGGTGGAGCAGCAGCAAGCAACCCCTGTCTGAGACTGGAGCCGAGG 1225
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Qy 1346 GGAGAGAACTCGCCAGCTGTGGAAAGAGACGAGCGTGTACACAGCAACCCCGGAACCA 1405
Db 1324 GGAGAGAAATGCTGGCCCTCTGGAAGAGATGCAACAGGCTCA----- 1367
Qy 1406 ACCAGGCATTCCGAGCAGCANTCCGCTGCTGCCAGAGAGCTCTT---AGAAGTGAGGGC 1462
Db 1368 -----CTGCAATCTCTGCTCTCCAGATGAGGTCTTGGAAAGAGCGAGGGC 1414
Qy 1463 TGTGACCCCTTCG-ATCCTGAGCGGCTAGTATTTCAAACCTCCCTTGGCCCTGCTTCTTC 1521
Db 1415 TGTGACCGTTCAGATCTGAGCGGCCAGCTTTCAAACCTCTCTCTAC-----TTACTC 1467
Qy 1522 TGGCTCAGGCTGCTCCTCCTTAGGACTTTGTGGGFCAGTTTGGCTTCTGTCTGTATGG 1581
Db 1468 CTGCTTGGGCTGCTCCTCCTTAGGACCTTGT-ACTCCAGTTTGGCTGTATATTGTGGTGG 1526
Qy 1582 TGATTAGGGCTCAGCTCAGGGCTTCTTCTGTTTCCAGGACCAACCCAGAGGCTAAGG 1641
Db 1527 TGATTAGCTTCCCACCTCAGGCCCTTCTTCTGTTTCCAGGACCAACCCAG-GGGTAATG 1585
Qy 1642 AATCAGTCAATTCCTGTTGCTTCTCCAGGAGGAGGCTAAGGGTCTGAGGTGACTGA 1701
Db 1586 ACTCACTCATTTCTGTTGCTTCTTCCAGGAGGAGGCTGAGGTTCTGAGGCGAGCTGA 1645
Qy 1702 GAAATATGTTTCTTGTGTGGAAGGCTGGTGTCTCCAGCC 1741
Db 1646 GAAAGATGCTCCTTTGTGTGAGGAAGGCTGGTGGTCCAAACC 1685
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RESULT 5

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US-09-828-366-15
; Sequence 15, Application US/09828366
; Patent No. US20020010137A1
; GENERAL INFORMATION:
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Napier, Mary
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; PRIOR FILING DATE: 2001-04-05
; Prior filing data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 15
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-828-366-15
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Query Match 48.3%; Score 934.6; DB 3; Length 1829;
Best Local Similarity 73.3%; Pred. No. 2.6e-272;
Matches 1357; Conservative 0; Mismatches 404; Indels 90; Gaps 9;
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Qy 83 CCGCCATGGGGCTCTCTGTGGAGCCCGGACCTC-----CACTGCTGATGATCTG 133
Db 32 CTCGCCATGGGCGCCCCCTCGAACCCGCGACCGCTGCCGCCGCTAGTCTCTGATGTGCTG 91
Qy 134 CTACTGTGTGTCTGTTGTGCTGCCACTTTGGAGCAGGAAATCTCCCTTTGCCACAGAGAAC 193
Db 92 CTGCTGTGCCGCGTCTGCCGCTGCTCTCGACGCGGAGACCCCTTCCACAGAAAGC 151
Qy 194 AGTTTGTGAACAGCTGTACCCAGGCCAGAAAGAAATGCGAGGCTAATCCCGCTTGCAG 253
Db 152 CGACTCATGAACAGCTGTCTCAGCGCAGGAGGAAGTCCAGGCTGATCCCACTGCAGT 211
Qy 254 GCTGCCCTACCAGCAGTGGGGCTCTGCACCTCCAGTTTAAAGCAGCGCGCTGCCCTTAGAG 313
Db 212 GCTGCCCTACCAGCAGTGGGATTTCTGCACCTCTTAGCATTAAGCACCCTGCCCTCAGAG 271
Qy 314 GAGTCTGCCATGTCTGCAGACTGCTAGAGCGACAGAAACAACTCAGGAAACAGCTCTCTG 373
Db 272 GAGCTTGGTCTCTGTGCTGCTGCTGAGGAGCAGCAAGCAACTCAGGAAACAGCTCTG 331
Qy 374 ATAGCTGAGGTTGCCATTCGGCGCATGAAGCA CCAAGTACCTGTCTGTGGAATTTATGG 433
Db 332 ATAGGCTGCATGTGCCACCGCGCATGAAGAAACAGGTTGCTGCTTGGACATCTATTGG 391
Qy 434 ACCGTTCAACCTCGCCCGAAGCCTTGGTGACTACGAGTTGGATGTCTCACCTATGAAAGAC 493
Db 392 ACCGTTCAACCTCGCCCGAGCCTTGGTAACTATGAGCTGGATGTCTCCCCCTATGAAGAC 451
Qy 494 ACAGTGACAGCAAAACCTCGAAATGAATCTTAGCAAGTTGAACATGCTCAAAACAGAC 553
Db 452 ACAGTGACAGCAAAACCTCGAAATGAATCTCAGCAAACTGAACATGCTCAAAACAGAC 511
Qy 554 TCGAACCTCTGCTCAAAATTTGTATGCTGTGTAATCTTCTCAGCAAGAGTGTGACGCGCTG 613
Db 512 TCAGACCTCTGCTCAAGTTTGCATCTGTGTACTCTCAATGAACAAGTGTGACGCGGCTG 571
Qy 614 CGCAAGGCTACGCGGAGGCGATGCTCAGGGATCCGCTGCGAGCGCCACCTCTGCTAGACC 673
Db 572 CGCAAGGCTACGCGGAGGCGGTGCTCCGGGCCCCACCTGCGCAGCGCCAGCTCTGCTCAGG 631
Qy 674 CAGCTGCGCTCTTCTTTTGAAGAGCAGAGTCCCAACGCTCAGGGTCTGCTGCTGTGT 733
Db 632 CAGCTGCTCACTTTCTTCGAGAAAGCGCCGAGCCCCCAGCGCGCAGGCGCTGCTACTGTGC 691
Qy 734 CCCTGTGCAACAGAAATGTGGGCTGTGGGAGGCGGCGGTGAACACCATCGCCCCCAGT 793
Db 692 CCATGTGCCCCCAACGACCGGGGCTGCGGGAGCGCGCGGCGCAACACCATCGCCCCCAGT 751
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Db 808 ACCCACTGCCATCCCATGACATCTAGGAATTTGTGCAACAGAGCAGTCCAGATGTCTA 867
Qy 947 CGGGCATACCTGGGGCTGATTTGGAGTGCATGACCCCAAACTTCATCAGCAAGTCAAC 1006
Db 868 CAGCATACCTGGGGCTGATTTGGAGTGCATGACCCCAAACTTTGTGCAAGTGTCAAC 927
Qy 1007 ATCTACTGTTGCCCTTAAGCTGCACTGCGGAGCAGCGGCAACCTACAGGACGAGTGTCAA 1066
Db 928 ACCAGTGTTCCTTAAGCTGCACTGCGGAGCAGTGCACCTGCAGGAGGAGTGTCAA 987
Qy 1067 CAGCTGGAAGGTCTCTTCCAGAACCCCTGCTGCTGGAGGCCATTCGAGCTAAAGATG 1126
Db 988 ATGCTGGAAGGTCTCTTCCCAACCCCTGCTGCTGAGGCCATTCGAGCTAAAGATG 1047
Qy 1127 CGTTTCCACAGACAGTCTTCTCCAGCACTGGGAGCAGTCTACTTTTTCAGTGTGTGCGAG 1186
Db 1048 CGTTTTCACAGCAAACTCTTCTCCAGCACTGGCCACACCCCTACCTTTTGTGTGATGGCA 1107
Qy 1187 CAGCAGAACAGCAACCCCTGCTGAGACTGCAGGCCAGGCTACCCCAATCTTTCTTTCTCC 1246
Db 1108 CACCAAGATGAACCCCTGCTGAGGCCACAGCCCTGGGTGCCCTCTCTTTTCTCCTGC 1167
Qy 1247 ATCTTCCCTGATTCCTGCTGAGACCTCTGCTGATG 1282
Db 1168 ACGCTTCCCTGATTCCTGCTGAGCCTATGCTAG 1203

RESULT 11

US-10-668-936-18
; Sequence 18, Application US/10668936
; Publication No. US20050080235A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..946
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-668-936-18

Query Match 38.8%; Score 751.6; DB 9; Length 1271;
Best Local Similarity 82.5%; Pred. No. 8e-217;
Matches 873; Conservative 0; Mismatches 184; Indels 1; Gaps 1;

Qy 344 GCAGCAGAACAACTCAGGAACAGCTCTCTGATAGACTGCGAGGTGCCATCGGCGCATGAAG 403
Db 11 GAAACACCTCAACTCAGGAACAGCTCTCTGATAGGTGCAATGTGCCACCGCGCATGAAG 70
Qy 404 CACCAAGCTACCTGCTGCGACATTTATTTGGACCGTTTCCACCTGCGCCGAAGCCTTGTGTGAC 463
Db 71 AACAGGTGCTGCTGCGACATCTATTTGGACCGTTTCCACCTGCGCGAGCCTTGTGTAAAC 130
Qy 464 TACGAGTTGGATGCTCAACCCCTATGAAGACACAGTGCAGCAAAACCCCTGGAATGAAT 523
Db 131 TATGAGCTGGATGCTCCCCCTATGAAGACACAGTGCAGCAAAACCCCTGGAATGAAT 190
Qy 524 CTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTATGCTG 583
Db 191 CTCAGCAAACTGAACATGCTCAAAACAGACTCAGACCTCTGCTCTCAAGTTTGGCCATGCTG 250
Qy 584 TGTACTCTTCAACGACAAAGTGTGACCGCTGCGCAAGGCTTACGGGAGGCAATGCTCAGGG 643
Db 251 TGTACTCTCAATGAAAGTGTGACCGCTGCGCAAGGCTTACGGGAGGCGTCTCCGGG 310
Qy 644 ATCCGCTGCCAGCGCCACCTCTGCTAGCCAGCTGGCTCTCTTTTGAAGAGGCAAGCA 703
Db 311 CCCCACTGCCAGCGCCAGCTCTGCTCAGGCAAGTCTGCTCTTTCGAGAAGGCGCC 370
Qy 704 GAGTCCCAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
Db 371 GAGCCCAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
Qy 764 GAGCGCGGCTTAACACCATCGCCCGCTTGGCGCTTCTGTAACCCCAATGTC 823
Db 431 GAGCGCGGCGCAACACATCGCCCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTG 490
Qy 824 CTGGATCTGGCGAGCTTCTGCGCTGCGGACCTTTTGTGCAAGATCACGCTGATGAGACTTC 883
Db 491 CTGGAGCTGCGGCGCTCTGCTTCTCGACCGCTTTTGCAGATCACGCTGCTGCTGCTGCTGCTG 550
Qy 884 CAGACCACTGCTCATCTTATGGAATCTCTTGGGACTTTGTGGAATCTTGTGCAAGTGCAGATGT 943
Db 551 CAGACCACTGCTCATCTTATGGAATCTCTTGGGACTTTGTGGAATCTTGTGCAAGTGCAGATGT 610
Qy 944 CTGCGGCGCATACCTGGGCGCTGATTTGGGACTGCCATGACCCCAACTTCATCAGCAAGTGC 1003
Db 611 CTACGAGCATACCTGGGCGCTGATTTGGGACTGCCATGACCCCAACTTTTGTGCAAGTGC 670
Qy 1004 AACACTACTGTTGCTTTAAGCTGCACTGCGGAGCAGCGCAACCTTACAGGACGAGTGT 1063
Db 671 AACACCACTGTTGCTTTAAGCTGCACTGCGGAGGCAAGTGGCAACCTTGCAGGAGGAGTGT 730
Qy 1064 GAAACGCTGGAAGGTCTCTTCCAGAACCCCTGCTGCTGCGAGGCGCATTTGCAGCTAAG 1123
Db 731 GAAATGCTGGAAGGTTCTTCTCCACAAACCCCTGCTGCTGCGAGGCGCATTTGCAGCTAAG 790
Qy 1124 ATGCGTTTCCACACAGACTCTTCTCCAGGACTGGGCAAGTCTTACTTTTTCAGTGTGTG 1183
Db 791 ATGCGTTTCCACACAGACTCTTCTCCAGGACTGGGCAAGTCTTACTTTTTCAGTGTGTG 850
Qy 1184 CAGCAGCAGAACAGCAACCCCTGCTCTGAGACTGCGAGCCCGAGGCTACCCATCTTTCTTTTC 1243

Db 851 GCACACCAAGATGAAGAACCTCTGTGTGGCCACAGCCCTGTGGTCTCTTTCTCC 910
Qy 1244 TCCATCTTCCCTTGAATCTGTGTGAGACCTCTGTGTAGTGGCTTCTCAGGGTCTT 1303
Db 911 TGCAGCTTCCCTTGAATCTGTGTGAGACCTGTGTAGTGGCTTCTCAGGGCCCTC 970
Qy 1304 TGTCTCTCCACACACACACCTGATTTGTGAGCTGTGTGTGGAGAGAACTCGCAGCC 1363
Db 971 T-TCCCTCCACACACACACCTGAGCTTGTGAGCCACAAAGGGGTGAGGAAGGACAGCA 1029
Qy 1364 TGTGAAGAGAGCAGGTGTCTACACAGCAACCCGGA 1401
Db 1030 GCAGGAAGAGGTGAGTGTGAGAGAGAGGACAGCA 1067

RESULT 12
US-10-621-855-16
; Sequence 16, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 09/272,835
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-621-855-16

Query Match 38.7%; Score 749.8; DB 9; Length 1837;
Best Local Similarity 68.7%; Pred. No. 3.3e-216;
Matches 1271; Conservative 0; Mismatches 397; Indels 183; Gaps 10;

Qy 83 CCCGCCATGGGCTCTCTGTGAGCCCGCAGCTC-----CACTGTGATGATCTCTG 133
Db 136 CTCGCCATGGTGGCGCCCTGAACCCGCGAGCGCTGCCCGCTAGTCTGTATGTTGCTG 195
Qy 134 CTACTGGTCTGTGTGTGGTGGCACTTGGAGCAGGAACCTCCCTTGCACAGAGAAC 193
Db 196 CTGTGCTCCCGCTGCGCGCTGTCTCTCGAGCGGAGACCCCTTCCCAAGAAAGC 255
Qy 194 AGGTTGTCAACAGCTGTACCCAGGCGAGAAAGAAATGCGAGCTAATCCCGCTTGCAG 253
Db 256 CGACTCATGACAGCTGTCTCAGGCGAGGAGAGTGCAGGCTGATCCCACTTGCAGT 315
Qy 254 GCTGCTTACAGCACTGGGCTCTGTGACCTTCAGTTTAAGCAGGCGCGCTTGCCTTAG 313
Db 316 GCTGCTTACCAACCTGGATCTTGTGACCTCTAGCATAAAGCACCCCACTGCGCTCAG 375
Qy 314 GAGTGTGCCATGTGTGACAGCTGCTAGAGGAGCGAGAACTCAGGACAGCTCTCTG 373
Db 376 GAGCTTCTGGTCTCTGCTGCTGCTGAGGAGGAGCAGCAACTCAGGAACAGCTCTCTG 435
Qy 374 ATAGACTGAGTGGCATCGGCGCATGAGAGCAAGCAAGCTGTGTGACATTTATTGG 433
Db 436 ATAGGCTGATGTGCGCACCGCGCATGAAGAACAGGTTGCTGTGAGCATCTATTGG 495
Qy 434 ACCGTTTCCCTGCGCGAGCTTGTGTGACTACGAGTTGGATGTCTCTCACCTTATGAAGAC 493

Db 496 ACCGTTACCGTGTGCCCGCAGCCTT----- 519
Qy 494 ACAGTGCACGAAACCCCTGGAATGAATCTTAGCAAGTTGAACATGCTCAAAACAGAC 553
Db 520 -----GAC 522
Qy 554 TCGAGACTCTGCTCAAAATTTGCTATGCTGTGTACTCTTACGACAAAGTGTGACGCGCTG 613
Db 523 TCAGACCTCTGCTCAAGTTTGGCATGCTGTGTACTCTCAATGACAAAGTGTGACGCGCTG 582
Qy 614 CGCAAGGCTTACGCGGAGGATGCTCAGGGATCGCTGCGCAGCGCCACTCTGCTGCTAGCC 673
Db 583 CGCAAGGCTTACGCGGAGGCTGTCTCGGGCCCACTGCGCAGCGCCAGCTGTGCTCAGG 642
Qy 674 CAGCTGCGCTCTCTTTTGAAGAGGACAGAGTCCACGCTCAGGGTCTGTGTGTGTGT 733
Db 643 CAGCTGCTCACTTTTCGAGAAGCCGCCGAGCCCAACGCGCGGAGGCTGTCTACTGTGC 702
Qy 734 CCCTGTGCAACAGAGATGCGGGCTGTGGGAGGGGCGGTAAACCATCGCCCCAGT 793
Db 703 CCATGTGCCCCCAACGACCGGGGCTGTGGGAGGCGCGCGCAACACCATCGCCCCAAC 762
Qy 794 TGGCGCTCTCTTGTAAACCCCAATTTGCTGTGATCTGCGAGCTTCTGCGCTGCGGAC 853
Db 763 TGGCGCTGCGCGCTGTGGCCCCCACTGCTGTGAGCTGCGGCGCTCTGTCTCCGAC 822
Qy 854 CTTTGTGAGATCACGCTGTGAGACTTCCAGACCCCACTGTCTCATCTATGAGACATCTT 913
Db 823 CCGCTTTGAGATCACGCTGTGTGATTTCCAGACCCCACTGCCATCCCATCGACATCTTA 882
Qy 914 GGGACTTGTGCAACTGAGCAGTCCAGATGTCTGGGGATACCTTGGGCTGATTTGGGACT 973
Db 883 GGAACCTTGTGCAACAGAGCAGTCCAGATGTCTAGGACATACCTTGGGCTGATTTGGGACT 942
Qy 974 GCCATGACCCCAACTTTCATCAGCAAGCTCAACTACTGTGTGCTTAAAGCTGCACCTGC 1033
Db 943 GCCATGACCCCAACTTTGTGAGCAATGTCAACACAGTGTGTGCTTAAAGCTGCACCTGC 1002
Qy 1034 CGAGGAGCGGCAACCTACAGGACGAGTGTGAAACAGCTGGAAGGCTCTTCTCCAGAAC 1093
Db 1003 CGAGGAGTGGCAACCTGCGAGGAGGTGTGAATGTCTGGAAGGCTTCTTCTCCCAAC 1062
Qy 1094 CCTGCTCTGTGGAGGCAATTTGCACTTAAGATGTGTTCACAGACAGCTCTTCTCCAG 1153
Db 1063 CCTGCTCTACGAGGCGCAATTTGCACTTAAGATGTGTTCACAGCAACTCTTCTCCAG 1122
Qy 1154 GACTGGGAGACTCTACTTTTTCAGTGTGTGAGCAGCAGCAAGCAACCTGCTCTGAGA 1213
Db 1123 GACTGGGCAACCCCTTACCTTTGTGTGATGCAACACAGATGAACCTTGTGTGAGG 1182
Qy 1214 CTGAGGCGGAGCTACCCATTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTGAGAC 1273
Db 1183 CCACAGCTCTGGTGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGAGC 1242
Qy 1274 CTCTGTGTGAGGCTCTTCTCAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1333
Db 1243 CTATGTGTGAGTGTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1301
Qy 1334 CAGCTGTGTGGGAGAGAACTCGCCAGCTGTGGAAGAGCAGCAGCTGTCTACAGC 1393
Db 1302 CAGCCCAACAGGGGTGAGGAAGGACAGCAGGAAGAGGTGAGTGTGCGCAGATGAGG 1361
Qy 1394 AACCGGAACCAACCCAGGCAATTCGCGAGCAGCATCCCGTCTGCTCCAGAAAGAGGTCTTAGA 1453
Db 1362 GCACAGG-----AGA 1371
Qy 1454 AGTGAAGGCTGTGACCTTCCGATCTCTGAGGCGGTAGTTTTCAAACCTTCTTCTTCTG 1513
Db 1372 AGCTAAGGGTTATGACCTTCCAGATCTTACTGTGTCCAGTCTCTTCTTCTTCTTCTT 1431
Qy 1514 CTTCTTCTTGGCTGAGGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1573
Db 1432 TCCACTTCTGTATCTATGCTGCGCCCTC-----CTTGTGGGCCCAAAATTAGCCATGCA 1484

QY 1574 TCTGATGGTATTAGCGGCTCACCTCC-----AGCGCTTCTTCCRGTTTCCAGGAC 1625
DB 1485 TCTGGTGGTACCAGCTCCACGAGCCCTTCTGAGCGCTTCTCTTGACTACAGGAT 1544
QY 1626 CACCAGAGGCTAAGGAATCAGTCAATCCCTGTGTGCTTC-----TCCAGGAAG 1674
DB 1545 CA-CCAGAATCTAATAAGTTAGCCCTTCTCTATTGCAATCCAGATTAGGGTTAGGGTAGG 1603
QY 1675 GCAGGCTAAGGGTCTGAGGTGACTGAGAGAAATGTT--TCTTTGTGTGGAGGCTGGTG 1733
DB 1604 GAGGACTGGGTGTCTGAGGAGCAGCTAGAAAGTCAATCTCTTTGTGAAGAGGCTCCTG 1663
QY 1734 CTCAGGCTCCACGCTCCCTCTGAATGGAAGATAAAACCTGCTGTGTCTTGACTGCTCT 1793
DB 1664 CCCCCTGCTCC--TCTCTGAGTGGAGGATGGAACACTACTGCTGCACGCTGCTGTC 1721
QY 1794 GCCAGGCAATCTGAACATTTGGGCATGAAGACTAAAGTCTTTGGGTCTTTTAACTC 1853
DB 1722 CCGGATCCTGCGAACAATCTGGGCATCAGGAGCTGGAGCCTGTGGGCTTGTCTTATTC 1781
QY 1854 CTATTACTGTCCCAAAATCCCTAGTCCCTTGGGTGATGATTAACAATTT 1904
DB 1782 CTATTATTGCTCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAACCTTT 1832

RESULT 13
US-10-621-855-1
; Sequence 1, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRLPH3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-621-855-1

Query Match 19.9%; Score 385.4; DB 9; Length 387;
Best Local Similarity 99.7%; Pred. No. 7e-106;
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1326 CTGATTGAGCTGTGTGGAGAGAACTGCGCAGCCTGTGGAAGAGAGCGAGCGTGC 1385
DB 1 CTGATTGAGCCTGTGTGGAGAGAACTGCGCAGCCTGTGGAAGAGAGCGAGCGGC 60
QY 1386 TACACAGCAACCCGGAACCAACCGGCATTCGCGAGCATCCGCTCTGCTCCAGAGAG 1445
DB 61 TACACAGCAACCCGGAACCAACCGGCATTCGCGAGCATCCGCTCTGCTCCAGAGAG 120
QY 1446 GTCTTAGAAGTGAGGCTGTGACCCCTTCGATCTCGATCGGCGTGTGTTTCAAACTCCCT 1505
DB 121 GTCTTAGAAGTGAGGCTGTGACCCCTTCGATCTCGATCGGCGTGTGTTTCAAACTCCCT 180
QY 1506 TGCCCCCTGCTCTTCTGGCTCAGGCTGCTCTCTTAGGACTTTTGTGGGTCCAGTTTG 1565
DB 181 TGCCCCCTGCTCTTCTGGCTCAGGCTGCTCTCTTAGGACTTTTGTGGGTCCAGTTTG 240

QY 1566 CTTTCTGTTCTGATGGTGATTAGCGGCTCACCTCCAGCGCTTCTTCTGTGTTTCCAGGAC 1625
DB 241 CTTTCTGTTCTGATGGTGATTAGCGGCTCACCTCCAGCGCTTCTTCTGTGTTTCCAGGAC 300
QY 1626 CACCAGAGGCTAAGGAATCAGTCAATCCCTGTGTGCTTCTCCAGGAAGGAGGCTAAGG 1685
DB 301 CACCAGAGGCTAAGGAATCAGTCAATCCCTGTGTGCTTCTCCAGGAAGGAGGCTAAGG 360
QY 1686 GTTCTGAGGTGACTGAGAAAAATGTTT 1712
DB 361 GTTCTGAGGTGACTGAGAAAAATGTTT 387
RESULT 14
US-10-621-855-2
; Sequence 2, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRLPH3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-621-855-2

Query Match 17.1%; Score 331; DB 9; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.2e-89;
Matches 353; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 37 CGCGCGCCAGCGCAGGCGCTGTCCATCCCGGGGCTCACCCGCGCATGGGGCT 96
DB 1 CGCGCGCCAGCG-AGGAGAGGCTGTCCATCCCGGGGCTCACCCGCGCATGGGGCT 59
QY 97 CTCCTGGAGCCCGGACCTCCACTGCTGATGATCCTGCTACTGTGTGTGTTGGCT 156
DB 60 CTCCTGGAGCCCGGACCTCCACTGCTGATGATCCTGCTACTGTGTGTGTTGGCT 119
QY 157 GCCACTTGGAGCAGGAACTCCCTTGGCAGAGAACAGGTTTGTGAACAGCTGTACCCA 216
DB 120 GCCACTTGGAGCAGGAACTCCCTTGGCAGAGAACAGGTTTGTGAACAGCTGTACCCA 179
QY 217 GGCCAGAGAAAGAACCGGAGCTTAATCCGCTTTCAGAGCTCCCTACAGCACCTGGGGCTC 276
DB 180 GGCCAGAGAAAGAACCGGAGCTTAATCCGCTTTCAGAGCTCCCTACAGCACCTGGGGCTC 239
QY 277 CTGCACCTCCAGTTTAAAGCAGGCGCTGCCCTTAGAGAGAGTCTGCCATGTCTGAGACTG 336
DB 240 CTGCACCTCCAG-TTAAAGCAGGCGCTGCCCTTAGAGAGAGTCTGCCATGTCTGAGACTG 298
QY 337 CCTAGAGCAGCAGAACATCTCAGAACAGCTCTCTGATAGACTGTCAGGTGCCAT 391
DB 299 CCTAGAGCAGCAGAACACTCAGAACAGCTCTCTGATAGACTGTCAGGTGCCAT 353

RESULT 15
US-10-305-720-530
; Sequence 530, Application US/10305720
; Publication No. US20040010136A1

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:22:40 ; Search time 663 Seconds
(without alignments)
6805.204 Million cell updates/sec

Title: US-10-621-855-4
Perfect score: 1935
Sequence: 1 Gaatttgcctcaggcca.....aaaaaaaaaaaaaaaaaa 1935

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues
Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	604.6	31.2	667	12	US-11-136-527-666
2	544	28.1	600	12	US-11-136-527-4762
3	265	13.7	784	12	US-11-136-527-1671
4	227.6	11.8	600	12	US-11-136-527-5767
5	86	4.4	2787	12	US-11-136-527-3767
6	72.6	3.8	1707	8	US-10-955-054A-193
7	72.6	3.8	2542	8	US-10-955-054A-9
8	67.8	3.5	3673	12	US-11-136-527-246
9	44	2.3	574	6	US-09-925-065A-573503
10	44	2.3	574	6	US-09-925-065A-573504
11	40.8	2.1	629	12	US-11-136-527-1281
12	40.2	2.1	1400	12	US-11-136-527-7487
13	40.2	2.1	1494	12	US-11-136-527-3391
14	39.8	2.1	1494	8	US-10-444-926-9
15	39.4	2.0	522	6	US-09-925-065A-319364
16	39.4	2.0	522	6	US-09-925-065A-319365
17	39.4	2.0	2357	8	US-10-947-249-99
18	39.2	2.0	613	6	US-09-925-065A-556194
19	38.6	2.0	153376	12	US-11-121-086-5
20	38.6	2.0	172543	12	US-11-121-086-6

c	21	38.2	2.0	2341	8	US-10-821-234-199	Sequence 199, App
	22	38	2.0	3020	8	US-10-947-249-155	Sequence 155, App
	23	37.8	2.0	1280	12	US-11-000-463-214	Sequence 214, App
	24	37.6	1.9	537	6	US-09-925-065A-499837	Sequence 499837,
	25	37.6	1.9	560	6	US-09-925-065A-498692	Sequence 498692,
	26	37.6	1.9	560	6	US-09-925-065A-949884	Sequence 949884,
	27	37.6	1.9	562	6	US-09-925-065A-499835	Sequence 499835,
	28	37.6	1.9	562	6	US-09-925-065A-499836	Sequence 499836,
	29	37.6	1.9	1278	12	US-11-000-463-95	Sequence 95, Appl
	30	37.2	1.9	562	6	US-09-925-065A-499834	Sequence 499834,
	31	37.2	1.9	1400	12	US-11-136-527-4809	Sequence 4809, Ap
	32	37.2	1.9	2124	12	US-11-136-527-713	Sequence 713, App
	33	37	1.9	482	6	US-09-925-065A-510953	Sequence 510953,
	34	37	1.9	535	6	US-09-925-065A-258873	Sequence 258873,
	35	37	1.9	567	6	US-09-925-065A-951524	Sequence 951524,
	36	37	1.9	579	6	US-09-925-065A-932296	Sequence 932296,
	37	37	1.9	579	6	US-09-925-065A-951523	Sequence 951523,
	38	37	1.9	585	6	US-09-925-065A-753184	Sequence 753184,
	39	37	1.9	647	12	US-11-000-463-230	Sequence 230, App
	40	37	1.9	1056	12	US-11-136-527-3921	Sequence 3921, Ap
	41	36.8	1.9	587	6	US-09-925-065A-826467	Sequence 826467,
	42	36.8	1.9	604	6	US-09-925-065A-659494	Sequence 659494,
	43	36.8	1.9	612	6	US-09-925-065A-767121	Sequence 767121,
	44	36.8	1.9	621	6	US-09-925-065A-740743	Sequence 740743,
	45	36.8	1.9	771	12	US-11-091-883-268	Sequence 268, App

ALIGNMENTS

RESULT 1

US-11-136-527-666
; Sequence 666, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 666
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-666

Query Match	31.2%	Score	604.6	DB	12	Length	667
Best Local Similarity	94.2%	Pred. No.	1.7e-126	Mismatches	0	Indels	0
Matches	628	Conservative	0	0	0	Gaps	0
Qy	493	CACAGTGACCAAGCAACCCCTGGAAATGAATCTTTAGCAAGTTGAACATGCTCAAAACGAGA	552				
Db	1	CACAGTGACCAAGCAACCCCTGGAAATGAATCTCAGCAAGCTGAGCATGCTCAAAACGAGA	60				
Qy	553	CTCGGACCTTGCCTCAAAATTTGCTATGCTGTGCTACTCTTCCAGCAAGTGTGACCGCT	612				
Db	61	CTCGGACCTTGCCTCAAAATTTGCTATGCTGTGCTACTCTTCCAGCAAGTGTGACCGCT	120				
Qy	613	CGCAAGGCTTACGGGAGGATGCTCAGGATTCGGTCCAGGCGCCACCTCTGCTTACG	672				
Db	121	CGCAAGGCTTACGGGAGGATGCTCAGGATTCGGTCCAGGCGCCACCTCTGCTTACG	180				
Qy	673	CCAGTGGCTCTCTTTTGAAGAGGAGAGTCCACGCTCAGGCTGTGCTGTGCTGTG	732				
Db	181	TCAGTGGCTCTCTTTTGAAGAGGAGAGTCCACGCTCAGGCTGTGCTGTGCTGTG	240				
Qy	733	TCCCTGTGCACCAAGATGCGGCTGTGGGAGGGGGGCTGTAACATGCCCCCGG	792				

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Db      241  TCCCTGTGCACCCGAAGATGCGGGCTGTGGGAGCGCGCGCAACACCATCGCCCCCAG 300
Qy      793  TTGGCCCTTGCCTTTCTGTAA CCCCCAAATTGCTGTGATCTGGGAGCTTCTGCCGTGGGA 852
Db      301  TTGGCCCTTGCCTTGTGGCCCCCAACTGCTAGATCTTCGGAGCTTCCGCCGTGGGA 360
Qy      853  CCCTTTGTGCAGATCACGCGCTGATGGACTTTCAGACCCCACTGTCTATCTATGGACATCCT 912
Db      361  CCCTCTGTGCAGATCAGCGCTGATGGACTTTCAGACCCCACTGTCCACCTATGGACATCCT 420
Qy      913  TGGGACTTGTGCACTGACGAGTCCAGATGTCTGGGGCATACCTCTGGGGCTGATTTGGGAC 972
Db      421  CGGGACTTGTGCAACTGAGCAGTCCAGATGTCTGGGGCATACCTCTGGGGCTAAATTGGGAC 480
Qy      973  TGCCATGACCCCAACTTTCATCAGCAAGGTCAACTACTGTCTGGCTTAAGCTGACCTG 1032
Db      481  TGCCATGACCCCAACTTTCATCAGCAAGGTCAACTACTGTCTGGCTTAAGCTGACCTG 540
Qy      1033  CCGAGCGAGCGCAACCTTACAGGAGAGTGTGAACAGCTGGAAAGTCTCTTCTCCAGAA 1092
Db      541  CCGAGCGAGTGGCAACCTTGCAGGACAGTGTGAACAGCTGGAAAGTCTCTTCTCCAGAA 600
Qy      1093  CCCCTGCTCTGTGGAGGCCATTGACGCTAAGATGCGTTTCCACAGACAGCTTCTTCCCA 1152
Db      601  CCCCTGCTCTCATGGAGGCCATTGCGGCTAAATGCGTTTCCACAGACAACTCTTCTCCCA 660
Qy      1153  GGACTGG 1159
Db      661  GGACTGG 667
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RESULT 2

US-11-136-527-4762
; Sequence 4762, Application US/11136527
; Publication No. US20050287570A1

GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4762
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-11-136-527-4762

Query Match 28.1%; Score 544; DB 12; Length 600;

Best Local Similarity 94.2%; Pred. No. 7.3e-113;

Matches 565; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy      560  CTCTGCCTCAAAATTGCTATGCTGTGTACTCTTACAGCAAGTGTGACGGCTTGGCAG 619
Db      1  CTCTGCCTCAAAATTGCTATGCTGTGTACTCTTAAAGCAGGTGGACGGCTTCCGAAAG 60
Qy      620  GCCTAGCGGGAGCGATGCTCAGGGATCGCTGCCAGCGCACCTCTGCTAGCCAGCTG 679
Db      61  GCCTAGCGGGAGCGGTGCTCAGGGATCGCTGCCAGCGCACCTCTGCTAGCTCAGCTG 120
Qy      680  CGCTCTCTTTTGAAGAAGCAGACAGTCCACGCTCAGGGTCTGCTGCTGTGTCCTGT 739
Db      121  CGCTCTCTTCTTGAAGAAGCGCAGAGTCCACGCTCAGGGCTGTGCTGTGTCCTGT 180
Qy      740  GCACGAGAGATCGGGCTGTGGGAGCGCGGCTTAACACCATCGCCCCCAGTTGGCC 799
Db      181  GCACCGGAAGATCGGGCTGTGGGAGCGCGGCAACACCATCGCCCCCAGTTGGCC 240
Qy      800  CTGCTTCTGTAAACCCCAATTGCTGTGATCTGCGGAGCTTCTGCGGTGCGGACCTTTG 859
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Db      241  CTCCCGCTGTGTGGCCCCCAACTGCTAGATCTTCGGAGCTTCCGCCGTGGGAGCCCTCTG 300
Qy      860  TGCAGATCACCGCTGTATGGACTTCCAGACCCCACTGTCTATCTATGGACATCCTTTGGGACT 919
Db      301  TGCAGATCACCGCTGTATGGACTTCCAGACCCCACTGTCTATCTATGGACATCCTTCGGGACT 360
Qy      920  TGTCAACTGAGCAGTCCAGATGTCTGGGGCATACCTCTGGGGCTGATTTGGGACTGCCATG 979
Db      361  TGTCAACTGAGCAGTCCAGATGTCTGGGGCATACCTCTGGGGCTAAATTGGGACTGCCATG 420
Qy      980  ACCCCAAACTTTCATCAGCAAGGTCAAACACTACTGTCTGGCTTAAGCTGACCTGCGGAGGC 1039
Db      421  ACCCCAAACTTTCATCAGCAAGGTCAAACACTACTGTCTGGCTTAAGCTGACCTGCGGAGGC 480
Qy      1040  AGCGGCAACCTTACAGGAGCAGTGTGAACAGCTGGAAAGTCTCTTCTCCAGACCTTCC 1099
Db      481  AGTGGCAACCTTGCAGGAGCAGTGTGAACAGCTGGAAAGTCTCTTCTCCAGACCTTCT 540
Qy      1100  CTCGTGGAGGCCATTGACGCTAAGATGCGTTTCCACAGACAGCTTCTTCCAGGACTGG 1159
Db      541  CTCATGGAGGCCATTGCGGCTAAATGCGTTTCCACAGACAACTCTTCTCCAGGACTGG 600
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RESULT 3

US-11-136-527-1671/c

; Sequence 1671, Application US/11136527
; Publication No. US20050287570A1

GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1671
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-11-136-527-1671

Query Match 13.7%; Score 265; DB 12; Length 784;

Best Local Similarity 72.6%; Pred. No. 4.8e-50;

Matches 451; Conservative 31; Mismatches 86; Indels 53; Gaps 10;

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Qy      1315  CCACACCCAGCACTGATTTGCGAGCCCTGTGTGGGAGAGAACTCGCCAGGCTGTGGAAGAAG 1374
Db      769  CTWCNCCWACCCGACTTGCAGCCTGTGATGGGAGAGAAATGCTGGCCTCTGGAAGAAG 710
Qy      1375  ACGGAGCTGTGTACACAGCAACCCCGGAACCAACAGGCAATTCGCGAGCAGACATCCCGTCTG 1434
Db      709  ATGCAACACGAGCTCACT-----GCACATCTCTGTCTG 679
Qy      1435  CTCCAGAGAGAGTCTT---AGAGTGGGGCTGTGACCCCTTC-CGATCCTGAGCGGCTAG 1490
Db      678  CTCCAGATGAGGTCTTGGMAGARGCGGGCTGTGACCGKKCAKSKTCTGAGCGGCCAG 619
Qy      1491  TTTTCAAAACCTTCCCTTGCCCTTCTGCTTCTGGCTCAGGGCTGTCTCTCTTAGGACTTT 1550
Db      618  CTTTCAAAACCTTCTCTAC-----TWACTCTGCTTGGGCTGTCTCTCTTAGGACCTT 566
Qy      1551  GTGGGTCCAGTTTGGCTTCTGCTGATGTGATAGGGGTCACTTCCAGCGGTCTT 1610
Db      565  GT-ACTCAGTTTGGCTGTATATTGTGGTGTGATTAGCTTCCCACTCCAGCCCTTCTT 507
Qy      1611  CTTGTTTCCAGGACCAACCCAGGCTAAGGAATCAGTCAATTCCCTGTTGCTTCTCCAG 1670
Db      506  CTTGTTTCCAGGACCAACCCAG-GGCTAATGACTCACTCACTTCTCTGGTTCCTTCTCCAG 448
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